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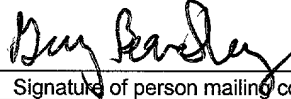
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Attorney's Docket Number:
00246/505003

TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

U.S. Application Number:
[UNKNOWN]

INTERNATIONAL APPLICATION NUMBER	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/US99/09034	27 April 1999	April 27, 1998
TITLE OF INVENTION:	REGULATION OF BIOFILM FORMATION	
APPLICANTS FOR DO/EO/US:	George A. O'Toole, Roberto Kolter	
Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:		
1.	<input checked="" type="checkbox"/> This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.	
2.	<input type="checkbox"/> This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.	
3.	<input checked="" type="checkbox"/> This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).	
4.	<input checked="" type="checkbox"/> A proper Demand for International Preliminary Examination was made by the 19 th month from the earliest claimed priority date.	
5.	A copy of the International Application as filed (35 U.S.C. 371(c)(2)). <input checked="" type="checkbox"/> a. is transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> b. has been transmitted by the International Bureau. <input type="checkbox"/> c. is not required, as the application was filed with the United States Receiving Office (RO/US).	
6.	<input type="checkbox"/> A translation of the International Application into English (35 U.S.C. 371(c)(2)).	
7.	Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)). <input type="checkbox"/> a. are transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> b. have been transmitted by the International Bureau. <input type="checkbox"/> c. have not been made; however, the time limit for making such amendments has NOT expired. <input type="checkbox"/> d. have not been made and will not be made.	
8.	Amendments to the claims of the International Application under PCT Article 34 <input checked="" type="checkbox"/> a. are transmitted herewith (required only if not transmitted by the International Bureau). <input type="checkbox"/> b. have been transmitted by the International Bureau. <input type="checkbox"/> c. have not been made; however, the time limit for making such amendments has NOT expired. <input type="checkbox"/> d. have not been made and will not be made.	
9.	<input type="checkbox"/> A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).	
10.	<input checked="" type="checkbox"/> An oath or declaration of the inventors (35 U.S.C. 371(c)(4)).	
11.	<input type="checkbox"/> A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).	
12.	<input type="checkbox"/> An Information Disclosure Statement under 37 CFR 1.97 and 1.98.	
13.	<input type="checkbox"/> An assignment for recording. A separate cover sheet in compliance with 37 3.28 and 3.31 is included.	

14.	<input type="checkbox"/> A FIRST preliminary amendment. <input type="checkbox"/> A SECOND or SUBSEQUENT preliminary amendment.		
15.	<input type="checkbox"/> A substitute specification.		
16.	<input type="checkbox"/> A change of power of attorney and/or address letter.		
17.	<input type="checkbox"/> Other items or information:		
18.	<div style="border: 1px solid black; padding: 5px;"> <input checked="" type="checkbox"/> The following fees are submitted: BASIC NATIONAL FEE (37 CFR 1.492(A)(1)-(5)): Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.455(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$ 1,000.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$ 860.00 International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$ 710.00 International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1) - (4) \$ 690.00 \$690.00 International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(1)-(4) \$ 100.00 </div>		
ENTER APPROPRIATE BASIC FEE AMOUNT =		\$690.00	
Surcharge of \$130 for furnishing the oath or declaration later than <input type="checkbox"/> 20 OR <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(e)).		\$	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE
Total claims	40 - 20 =	20	x \$18.00
Independent claims	11 - 3 =	8	x \$80.00
Multiple dependent claims (if applicable)			+ \$270.00
TOTAL OF ABOVE CALCULATIONS =		\$1,960.00	
Reduction of 1/2 for filing by small entity, if applicable. Verified Small Entity Statement must also be filed with this request (Note 37 CFR 1.9, 1.27, 1.28).		\$980.00	
SUBTOTAL =		\$ 980.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 OR <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492(f)).		+	\$
TOTAL NATIONAL FEE =		\$ 980.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). \$40.00 per property.		+	\$
TOTAL FEES ENCLOSED =		\$ 980.00	
		Amount to be refunded	\$
		charged	\$

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528 Rec'd PCT/PTO 17 OCT 2000

- ☒ a. A check in the amount of \$ 980.00 to cover the above fees is enclosed.
☐ b. Please charge my Deposit Account No. 03-2095 in the amount of \$ [**. **] to cover the above fees.
☒ c. The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment, to Deposit Account No. 03-2095.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

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Signature

Kristina Bieker-Brady, Ph.D.
Reg No. 39,109

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ATTORNEY DOCKET NO. 00246/505003

Applicant or Patentee : George A. O'Toole et al.
Serial or Patent No. :
Filed or Issued : October 17, 2000
Title : REGULATION OF BIOFILM FORMATION

**VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) and 1.27(d)) - NONPROFIT ORGANIZATION**

I hereby declare that I am an official empowered to act on behalf of the nonprofit organization identified below:

Name of Organization: President and Fellows of Harvard College

Address of Organization: 17 Quincy Street, Cambridge, MA 02138

Type of Organization:

- ☒ University or Other Institution of Higher Education
☐ Tax Exempt under Internal Revenue Service Code (26 USC 501(a) and 501(c)(3))
☐ Nonprofit Scientific or Educational under Statute of State of the United States of America
Name of State:
Citation of Statute:
☐ Would Qualify as Tax Exempt under Internal Revenue Service Code (26 USC 501(a) and 501(c)(3)) if Located in the United States of America
☐ Would Qualify as Nonprofit Scientific or Educational under Statute of State of the United States of America if Located in the United States of America
Name of State:
Citation of Statute:

I hereby declare that the nonprofit organization identified above qualifies as a nonprofit organization as defined in 37 CFR 1.9(e) for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code with regard to the invention entitled REGULATION OF BIOFILM FORMATION by inventors George A. O'Toole and Roberto Kolter described in

- ☒ the specification filed herewith.
☐ application serial no. _____, filed _____
☐ patent no. ["PATENT NUMBER"], issued ["ISSUE DATE"].

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization with regard to the above identified invention.

If the rights held by the nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(c) or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d) or a nonprofit organization under 37 CFR 1.9(e).

*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

Full Name: Microbia Inc.

Address: One Kendall Square, Building 1400W, Suite 1418, Cambridge, MA 02139

☐ INDIVIDUAL ☒ SMALL BUSINESS CONCERN ☐ NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name: Jeffrey Labovitz, Ph.D.

Title: Director, Office for Technology Licensing

Address: Harvard Medical School, Office of Technology Licensing & Industry Sponsored Research, 25 Shattuck Street, Building A, Room 414, Boston, MA 02115

Signature: 

Date: 10/13/2000

00246.505003 Small Entity Statement.wpd

ATTORNEY DOCKET NO. 00246/505003

Applicant or Patentee : George O'Toole et al.
Serial or Patent No. :
Filed or Issued : October 17, 2000
Title : REGULATION OF BIOFILM FORMATION

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS
(37 CFR 1.9(f) and 1.27(e)) - SMALL BUSINESS CONCERN

I hereby declare that I am

- ☐ the owner of the small business concern identified below:
☒ an official of the small business concern empowered to act on behalf of the concern identified below:

Name of Small Business Concern: Microbia Inc.

Address of Small Business Concern: One Kendall Square, Building 1400W, Suite 1418, Cambridge, MA 02139

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 CFR 121.12, and reproduced in 37 CFR 1.9(d), for purposes of paying reduced fees to the United States Patent and Trademark Office, in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention, entitled REGULATION OF BIOFILM FORMATION by inventors George O'Toole and Roberto Kolter described in

- ☒ the specification filed herewith,
☐ application serial no. _____, filed _____
☐ patent no. ["PATENT NUMBER"], issued ["ISSUE DATE"].

If the rights held by the above identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who would not qualify as an independent inventor under 37 CFR 1.9(e) if that person made the invention, or by any concern which would not qualify as a small business concern under 37 CFR 1.9(d), or a nonprofit organization under 37 CFR 1.9(e). NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

Assignee Name: President and Fellows of Harvard College
Assignee Address: 17 Quincy Street, Cambridge, MA 02138

☐ INDIVIDUAL ☐ SMALL BUSINESS CONCERN ☒ NONPROFIT ORGANIZATION

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent on which this verified statement is directed.

Name: Peter Hecht, Ph.D.

Title: President and CEO

Address: Microbia, Inc., One Kendall Square, Building 1400W, Suite 1418, Cambridge, MA 02139

Signature: 

Date: 10/16/00

09/673605

REGULATION OF BIOFILM FORMATIONStatement as to Federally Sponsored Research

5 This research has been sponsored in part by NIH grant number
GM58213 and NSF grant number 9207323. The government has certain rights
to the invention.

Field of the Invention

The field of the invention is bacterial genetics.

10

Background of the Invention

Populations of surface-attached microorganisms, comprised either of
single or multiple species, are commonly referred to as biofilms. In most
natural, clinical, and industrial settings, bacteria are found predominantly in
biofilms, not as planktonic cells such as those typically studied in the
15 laboratory. Biofilm bacteria display a different gene expression pattern,
different cellular physiology, and higher resistance to antibiotics, relative to
their planktonic counterparts.

Numerous reports have documented the ability of diverse bacterial
species to form biofilms on a variety of abiotic surfaces of great importance in
20 medicine and industry. For example, *Pseudomonas aeruginosa*, an organism
that causes nosocomial infections, forms biofilms on surfaces as diverse as
cystic fibrosis lung tissue, contact lenses, and catheter lines. In general,
biofilms can become hundreds of microns in depth, thereby clogging tubular
structures such as catheters and industrial pipes.

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Biofilm development initiates when bacteria make the transition from a planktonic existence to a lifestyle in which the microorganisms are firmly attached to biotic or abiotic surfaces. This transition is thought to be regulated in part by the nutritional status of the environment. After their initial attachment to the substratum, the cells are believed to undergo a program of physiological changes that result in a highly structured, sessile microbial community. After growth and development of the biofilm, the developmental cycle is completed when planktonic cells are shed from the biofilm into the medium, perhaps in response to a lack of sufficient nutrients (Costerton, J.W., et al., 1995, In *Annu. Rev. Microbiol.* Ornston, L.N., et al. (eds.). Palo Alto, CA: Annual Reviews, Inc., pp. 711-745; Wimpenny, J.W.T. and Colasanti, R., 1997, *FEMS Microbiol. Ecology* 22: 1-16).

Previous studies exploring biofilm formation have generally focused on identification of the organisms that comprise biofilms, their physical and chemical properties, and biofilm architecture (Costerton, J.W., et al., 1995, *supra*). In contrast, little is known about the cellular factors and molecular mechanisms required for the transition from a planktonic to a sessile mode of life and the subsequent development of a biofilm.

Understanding the molecular factors that contribute to biofilm initiation and maintenance would allow us to better control biofilm formation, and would thereby have a significant impact upon medicine, industry, and the environment.

Summary of the Invention

Using *Pseudomonas fluorescens*, *Escherichia coli*, and *Pseudomonas aeruginosa* as model organisms, we have investigated the molecular mechanisms required for biofilm formation. We have identified nutritional

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conditions that modulate biofilm formation in wild-type bacteria and in mutants defective in biofilm formation, and have identified a class of genes involved in biofilm formation, designated *surface attachment defective* (*sad*). The *sad* genes, *sad* gene products, and *sad* transcriptional control regions may all be used for the control of biofilm formation in commercially important fields such as manufacturing, agriculture, and healthcare. Furthermore, these reagents may be used in methods for the detection of industrially and pharmaceutically useful compounds for the modulation of biofilm formation.

In a first aspect, the invention features a purified nucleic acid. The purified nucleic acid includes a region that hybridizes under high stringency conditions to a probe containing at least 75 consecutive nucleotides that are complementary to a portion of an *n-sad* gene, wherein the region contains at least 75 consecutive nucleotides. In preferred embodiments of this aspect of the invention the *n-sad* gene is a *P. fluorescens sad* gene including a sequence chosen from SEQ ID NOs: 1-24, or the nucleic acid is contained within an expression vector.

In another preferred embodiment of the first aspect of the invention, the nucleic acid encodes a polypeptide that has a biological activity necessary for biofilm formation under at least one condition known to allow biofilm formation by a bacterium that expresses said polypeptide.

In a second aspect, the invention features a probe comprising at least 18 nucleotides that are complementary to an *n-sad* gene from *P. fluorescens* including a sequence chosen from SEQ ID NOs: 1-24. In preferred embodiments of this aspect of the invention, the probe includes at least 25, 40, 60, 80, 120, 150, 175, or 200 nucleotides that are complementary to the *n-sad* gene.

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In a third aspect, the invention features a substantially pure *n-sad* polypeptide. In a preferred embodiment of the second aspect of the invention, the polypeptide has a biological activity necessary for biofilm formation under at least one condition known to allow biofilm formation by a bacterium that
5 expresses the polypeptide.

In a fourth aspect, the invention features a substantially pure antibody that specifically binds an *n-sad* polypeptide.

In preferred embodiments of the third and fourth aspects of the invention, the polypeptide includes a polypeptide encoded by a *P. fluorescens*
10 *n-sad* gene that includes a sequence chosen from SEQ ID NOs: 1-24.

In a fifth aspect, the invention features a method of screening for a compound that modulates biofilm formation including a) contacting a sample containing a *sad* gene, *sad*/reporter gene fusion, or *sad* polypeptide with a test compound, and b) measuring the level of *sad* biological activity in the sample.
15 An increase in *sad* biological activity in the sample, relative to *sad* biological activity in a sample not contacted with the test compound, indicates a compound that increases biofilm formation. A decrease in *sad* biological activity in the sample, relative to *sad* biological activity in a sample not contacted with the test compound, indicates a compound that decreases biofilm
20 formation. In preferred embodiments, the sample comprises bacterial cell extract; the *sad* gene, the *sad*/reporter gene, or the *sad* polypeptide is within a bacterial cell; the *sad* gene, the *sad*/reporter gene, or the *sad* polypeptide are from *P. fluorescens*, and the *sad* gene and the *sad*/reporter gene include a sequence chosen from SEQ ID NOs: 1-24, or the *sad* polypeptide is encoded by
25 a gene comprising a sequence chosen from SEQ ID NOs: 1-24.

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In a sixth aspect, the invention features a method of screening for a compound that modulates biofilm formation including a) contacting a sample with a test compound, wherein the sample contains a *clpP* gene, a *clpP*/reporter gene, or a ClpP polypeptide, and b) measuring the level of ClpP activity in the sample. An increase in ClpP activity in the sample, relative to ClpP activity in a sample not contacted with the test compound, indicates a compound that increases biofilm formation. A decrease in ClpP activity in the sample, relative to ClpP activity in a sample not contacted with the test compound, indicates a compound that decreases biofilm formation. In preferred embodiments, the sample comprises bacterial cell extract; the *clpP* gene, the *clpP*/reporter gene, or the ClpP polypeptide is within a bacterial cell; the *clpP* gene, the *clpP*/reporter gene, or the ClpP polypeptide is from *P. fluorescens*; the ClpP activity is measured by measuring biofilm formation; or the *clpP* gene, *clpP*/reporter gene, or ClpP polypeptide is a non-*E. coli clpP* gene, a non-*E. coli clpP*/reporter gene, or a non-*E. coli* ClpP polypeptide.

In another preferred embodiment of the sixth aspect of the invention, the *clpP* gene, *clpP*/reporter gene, or ClpP polypeptide is within a bacterial cell and the bacterial cell is cultured under standard biofilm assay conditions after the contacting.

In a seventh aspect, the invention features a method for preventing a bacterial cell from participating in formation of a biofilm. The method may include any one of the following: inhibiting the synthesis or function of a *sad* polypeptide; inhibiting protein synthesis in the bacterial cell; contacting bacterial cell with a protease, where the contacting is sufficient to prevent the bacterial cell from participating in formation of a biofilm; limiting the concentration of $\text{Fe}^{2+}/\text{Fe}^{3+}$ in the environment of the bacterial cell, where the $\text{Fe}^{2+}/\text{Fe}^{3+}$ concentration of the environment is limited to 0.3 μM or less;

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providing a high osmolarity environment to the bacterial cell, where the osmolarity of the environment is equivalent to or greater than the osmolarity of a solution containing 0.2 M NaCl or 15% sucrose; and adding mannose to the environment of the bacterial cell, such that the mannose concentration in the environment after the addition of the mannose is at least 15 mM; and adding α -methyl-D-mannoside to the environment of the bacterial cell, such that the α -methyl-D-mannoside concentration in the environment after the addition of the α -methyl-D-mannoside is at least 15 mM.

In preferred embodiments the *sad* polypeptide is encoded by a *P. fluorescens sad* gene; the mannose concentration or the α -methyl-D-mannoside concentration is at least 15 mM, 25 mM, 50 mM, or most preferably 100 mM; or the surface is an abiotic surface.

In further embodiments of aspects 5, 6, and 7, the bacterial cell is selected from the group including: *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus* species, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, and other coagulase-negative *Staphylococcus* species, such as *S. hominis*, *S. haemolyticus*, *S. warneri*, *S. cohnii*, *S. saprophyticus*, *S. capitis*, and *S. lugdunensis*.

In an eighth aspect, the invention features a method for inhibiting participation of a bacterium in formation of a biofilm on a surface. The method includes inhibiting the synthesis or function of a flagellum on the bacterium. In preferred embodiments the surface is abiotic; or the synthesis or function of the flagellum is inhibited by inhibiting the synthesis or function of: FliC (Genbank Accession No. L07387 (gb-L07387); SEQ ID NO: 34); FlhD (gb-AE000283, U00096; SEQ ID NO: 35); MotA (gb-J01652; SEQ ID NO: 36); MotB (gb-M12914; SEQ ID NO: 37); FliP (gb-L22182, L21994; SEQ ID NO: 38); FlaE

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(gb-D90834, AB 001340; SEQ ID NO: 39); or FlgK (gb-AE000209, U00096; SEQ ID NO: 40); or homologues thereof. In another preferred embodiment of the eighth aspect of the invention, the inhibiting is under conditions that otherwise result in biofilm formation.

5 In a ninth aspect, the invention features a method for inhibiting participation of a bacterium in formation of a biofilm on an abiotic surface. The method includes inhibiting the synthesis or function of a pilus on the bacterium. In preferred embodiments the function of the pilus is inhibited by contacting the pilus with mannose or α -methyl-D-mannoside; the synthesis or
10 function of the pilus is inhibited by inhibiting the synthesis or function of: PilB (Genbank Accession No. M32066 (gb-M32066); SEQ ID NO: 41); PilC (gb-M32066; SEQ ID NO: 42); PilD (gb-M32066; SEQ ID NO: 43); PilV (gb-L76605; SEQ ID NO: 44); PilW (gb-L76605; SEQ ID NO: 45); PilX (gb-L76605; SEQ ID NO: 46); PilY1 (gb-L76605; SEQ ID NO: 47); PilY2 (gb-L76605; SEQ ID NO: 48); or PilE (gb-L76605; SEQ ID NO: 49); or
15 homologues thereof. In preferred embodiments, the bacterium is chosen from the group including: *Pseudomonas fluorescens*, *P. aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus* species, *Serratia marcescens*, *Staphylococcus aureus*,
20 *Staphylococcus epidermidis*, and other coagulase-negative *Staphylococcus* species, such as *S. hominis*, *S. haemolyticus*, *S. warneri*, *S. cohnii*, *S. saprophyticus*, *S. capitis*, and *S. lugdunensis*.

In a tenth aspect, the invention features a method of screening for a compound that inhibits bacterial pathogenicity. The method includes a)
25 exposing a bacterial culture to a test compound, such that at least one bacterial cell in the bacterial culture is contacted by the test compound, and b) testing the bacterial culture for biofilm formation on an abiotic surface. A decrease in

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biofilm formation, relative to biofilm formation by a bacterial culture that has not been exposed to the test compound, indicates a compound that inhibits biofilm formation, and an increase in biofilm formation, relative to biofilm formation by a bacterial culture that has not been exposed to the test compound, indicates a compound that stimulates biofilm formation. In preferred embodiments the bacterial culture is a liquid bacterial culture; at least 5%, 10%, 25%, 50%, 75%, or most preferably 100% of the bacterial cells contacted by the bacterial growth medium are contacted by the test compound; and the bacterial cell is chosen from the group including: *P. aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus* species, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, and other coagulase-negative *Staphylococcus* species, such as *S. hominis*, *S. haemolyticus*, *S. warneri*, *S. cohnii*, *S. saprophyticus*, *S. capitis*, and *S. lugdunensis*.

In an eleventh aspect, the invention features a method of stimulating formation of a biofilm by a population of bacteria. The method includes at least one of: adding iron to the growth environment of the bacteria, such that the final concentration of iron in the growth environment is at least 3 μ M; adding glutamate to the growth environment of the bacteria, such that the final concentration of glutamate in the growth environment is at least 0.4%; adding citrate to the growth environment of the bacteria, such that the final concentration of citrate in the growth environment is at least 0.4%; and stimulating expression of a *sad* gene or activity of a *sad* polypeptide. In a preferred embodiment, the bacterium is *Pseudomonas fluorescens*.

By "biofilm" is meant a sessile population of microorganisms, comprised of a single species or multiple species, that are enclosed by an extracellular matrix and adhere to each other and to a biotic or abiotic surface.

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By "standard biofilm assay" is meant experimental conditions that provide the equivalent to growth, on an abiotic surface, of approximately 10^6 colony forming units (CFU)/ml for 10 hours or 10^8 CFU/ml for approximately 30 minutes, at 30-37° C, preferably at 25° C, 30° C, or 37° C, in minimal M63 medium supplemented with 0.2% glucose and 0.5% casamino acids (CAA) or (particularly for *E. coli*) in rich medium such as Luria broth or Luria-Bertani broth.

By "environment" is meant the habitat or living conditions of a population of bacteria.

By "*sad* gene" or "surface attachment defective gene" is meant a DNA molecule that hybridizes at high stringency to one of the *sad* gene identifier sequences shown in Fig. 9, and encodes a polypeptide involved in biofilm formation on an abiotic surface under at least some environmental conditions. Examples of *sad* genes include the *P. fluorescens* genes *sad-10*, *sad-11*, *sad-13*, *sad-14*, *sad-16*, *sad-18*, *sad-19*, *sad-20*, *sad-21*, *sad-22*, *sad-51*, *sad-52*, *sad-53*, *sad-57*, *sad-58*, *sad-62*, *sad-79*, *sad-80*, *sad-81*, *sad-83*, *sad-87*, *sad-89*, *sad-98*, *sad-100*, *sad-101*, and *sad-102*.

By "*sad* polypeptide" is meant the protein product encoded by a *sad* gene.

By "*n-sad* gene" or "*n-sad* polypeptide" is meant a novel *sad* gene or gene product, including the *P. fluorescens* genes *sad-10*, *sad-11*, *sad-16*, *sad-18*, *sad-19*, *sad-20*, *sad-21*, *sad-22*, *sad-51*, *sad-52*, *sad-53*, *sad-57*, *sad-58*, *sad-62*, *sad-79*, *sad-80*, *sad-81*, *sad-83*, *sad-87*, *sad-89*, *sad-98*, *sad-100*, *sad-101*, and *sad-102*, and products of these genes.

By "*sad* gene identifier sequence" is meant a nucleotide sequence that constitutes a portion of a *sad* gene. A *sad* gene identifier sequence is at least 40 nucleotides, preferably at least 75 nucleotides, more preferably at least

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125 nucleotides, and most preferably at least 175 nucleotides. *Sad* gene identifier sequences include SEQ ID NOs: 1-24, shown in Fig. 9.

By "*sad* mutant" is meant a bacterium that has a mutation in a *sad* gene and is defective for biofilm formation. A *sad* mutant may be defective for biofilm formation on only a subset of surfaces, or on all surfaces. For example, the *sad-10* mutant described below has a biofilm formation defect on hydrophobic surfaces such as PVC, polycarbon, and polypropylene, but forms biofilms indistinguishable from wild-type biofilms on a hydrophilic surface such as borosilicate glass.

By "reporter gene" is meant any gene that encodes a product whose expression is detectable and/or quantifiable by immunological, chemical, biochemical or biological assays. A reporter gene product may, for example, have one of the following attributes, without restriction: fluorescence (e.g., green fluorescent protein), enzymatic activity (e.g., lacZ/ β -galactosidase, luciferase, chloramphenicol acetyltransferase), toxicity (e.g., ricin A), or an ability to be specifically bound by a second molecule (e.g., biotin or a detectably labelled antibody). It is understood that any engineered variants of reporter genes, which are readily available to one skilled in the art, are also included, without restriction, in the forgoing definition.

By "*sad*/reporter gene" or "*clpP*/reporter gene" is meant a DNA construct comprising transcriptional control sequences from, respectively, a *sad* gene or a *clpP* gene, operably linked to a reporter gene such that reporter gene expression is regulated in a manner analogous to that of an endogenous *sad* or *clpP* gene; therefore, modulation of expression of a *sad*/reporter or *clpP*/reporter gene construct, e.g., by a compound or environmental stimulus reflects modulation of expression of the endogenous *sad* or *clpP* gene. A

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sad/reporter or *clpP*/reporter gene may exist within a cell as an episomal DNA molecule, or may be integrated into the cellular genomic DNA.

By "*sad*/reporter mRNA," "*sad*/reporter polypeptide," "*clpP*/reporter mRNA," and "*clpP*/reporter polypeptide," is meant, respectively, the mRNA or
5 polypeptide encoded by a *sad*/reporter gene or a *clpP*/reporter gene.

By "changes in *sad* biological activity" is meant changes in:
transcription of a *sad* gene or *sad*/reporter gene; post-transcriptional
degradation or translation of a *sad* mRNA or *sad*/reporter mRNA; post-
translational degradation, enzymatic function, or structural function of a *sad*
10 polypeptide or *sad*/reporter polypeptide. In all cases, a change in *sad* biological
activity in a sample, for example, a sample exposed to an environmental
stimulus such as a change in nutrient status or the addition of a chemical, is
measured by an increase or decrease, in the activity being measured, of at least
30%, more preferably at least 40%, still more preferably at least 55%, and most
15 preferably by at least 70%, relative to a sample not exposed to the
environmental stimulus.

By "ClpP polypeptide" is meant any protease that bears at least 70%
sequence identity, more preferably at least 80%, and most preferably at least
89% sequence identity, over an amino acid stretch at least 50 amino acids in
20 length, to the *P. fluorescens* ClpP polypeptide. One example of a ClpP
polypeptide is the *E. coli* ClpP.

By "*clpP* gene" is meant any gene that encodes a ClpP protease.

By "ClpP activity" is meant enzymatic activity of Clp protease, as
evidenced by cleavage of a Clp protease substrate, for example, a misfolded
25 protein, RpoS, IO protein, and Mu vir repressor. ClpP activity may directly
measured by measuring Clp enzymatic activity. ClpP activity also may be
determined by measuring *clpP* mRNA levels or ClpP polypeptide levels, which

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reflect relative changes in: transcription of a *clpP* gene, post-transcriptional degradation of a *clpP* mRNA, translation of a *clpP* mRNA, or post-translational degradation of a ClpP polypeptide. In all cases, a change in ClpP activity in a sample, for example, a sample exposed to an environmental stimulus such as a change in nutrient status or the addition of a chemical, is measured by an increase or decrease of at least 30%, more preferably at least 40%, still more preferably at least 55%, and most preferably by at least 70%, relative to a sample not exposed to the environmental stimulus.

By "non-*E. coli* ClpP" or "non-*E. coli clpP*" is meant a ClpP polypeptide or nucleic acid that is not the ClpP polypeptide or nucleic acid that is naturally encoded by the endogenous *E. coli* genome.

By "homologue" is meant a gene (e.g., a gene encoding a polypeptide component of pili or flagella, or a polypeptide that regulates synthesis or function of pili or flagella) whose nucleic acid hybridizes at low stringency to the nucleic acid of a reference gene, and whose encoded polypeptide displays a biological activity similar to that of the polypeptide encoded by the reference gene. For example, the *Vibrio parahaemolyticus flaE*, *Salmonella typhimurium flgK*, and *P. fluorescens sad-14* genes are homologues of one another. The effect of a homologue on synthesis of pili or flagella may be assessed by measuring mRNA or polypeptide levels of pilus or flagellum components. Function of pili or flagella may be measured by motility assays, such as those known in the art and described herein.

By "biological activity" is meant an activity associated with biofilm formation, as provided herein below.

By "high stringency conditions" is meant conditions that allow hybridization comparable with the hybridization that occurs during an overnight incubation using a DNA probe of at least 500 nucleotides in length,

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in a solution containing 0.5 M NaHPO₄, pH 7.2, 7% SDS, 1 mM EDTA, 1% BSA (fraction V), and 100 µg/ml denatured, sheared salmon sperm DNA, at a temperature of 65° C, or a solution containing 48% formamide, 4.8X SSC (150 mM NaCl, 15 mM trisodium citrate), 0.2 M Tris-Cl, pH 7.6, 1X Denhardt's solution, 10% dextran sulfate, 0.1% SDS, and 100 µg/ml denatured, sheared salmon sperm DNA, at a temperature of 42° C (these are typical conditions for high stringency Northern or Southern, or colony hybridizations). High stringency hybridization may be used for techniques such as high stringency PCR, DNA sequencing, single strand conformational polymorphism analysis, and *in situ* hybridization. The immediately aforementioned techniques are usually performed with relatively short probes (e.g., usually 16 nucleotides or longer for PCR or sequencing, and 40 nucleotides or longer for *in situ* hybridization). The high stringency conditions used in these techniques are well known to those skilled in the art of molecular biology, and may be found, for example, in F. Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1997, hereby incorporated by reference.

By "low stringency" is meant conditions that allow hybridization comparable with the hybridization that occurs during an overnight incubation at 37°C using a DNA probe of at least 500 nucleotides in length, in a solution containing 20% formamide, 5X SSC, 50 mM sodium phosphate (pH 7.6), 5X Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA (these are typical conditions for low stringency Northern, Southern, or colony hybridizations). Low stringency hybridization may be used for techniques such as low stringency PCR, which is usually performed with relatively short probes (e.g., usually 16 nucleotides). Factors that alter hybridization stringency (e.g., the relative likelihood of forming a duplex

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between a single stranded probe and a target nucleic acid) are well known in the art, and are described in Ausubel, *supra*, at pages 2.10.8-2.10.16.

By "probe" or "primer" is meant a single-stranded DNA or RNA molecule of defined sequence that can base-pair to a second DNA or RNA molecule that contains a complementary sequence (the "target"). The stability of the resulting hybrid depends upon the extent of the base-pairing that occurs. The extent of base-pairing is affected by parameters such as the degree of complementarity between the probe and target molecules and the degree of stringency of the hybridization conditions. The degree of hybridization stringency is affected by parameters such as temperature, salt concentration, and the concentration of organic molecules such as formamide, and is determined by methods known to one skilled in the art. Probes or primers specific for nucleic acid encoding a *sad* gene preferably have at least 40% sequence identity, more preferably at least 45-55% sequence identity, even more preferably at least 60-75% sequence identity, still more preferably at least 80-90% sequence identity, and most preferably 100% sequence identity. Probes may be detectably-labelled, either radioactively, or non-radioactively, by methods well-known to those skilled in the art. Probes are used for methods involving nucleic acid hybridization, such as: nucleic acid sequencing, nucleic acid amplification by the polymerase chain reaction, single stranded conformational polymorphism (SSCP) analysis, restriction fragment polymorphism (RFLP) analysis, Southern hybridization, Northern hybridization, *in situ* hybridization, and electrophoretic mobility shift assay (EMSA).

By "identity" is meant that a polypeptide or nucleic acid sequence possesses the same amino acid or nucleotide residue at a given position, compared to a reference polypeptide or nucleic acid sequence to which the first

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sequence is aligned. Sequence identity is typically measured using sequence analysis software with the default parameters specified therein, such as the introduction of gaps to achieve an optimal alignment (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705).

By "substantially identical" is meant a polypeptide or nucleic acid exhibiting, over its entire length, at least 40%, preferably at least 50- 85%, more preferably at least 90%, and most preferably at least 95% identity to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences is at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably at least 35 amino acids. For nucleic acids, the length of comparison sequences is at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably at least 110 nucleotides.

By "substantially pure polypeptide" is meant a polypeptide (or a fragment thereof) that has been separated from the components that naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the polypeptide is a *sad* polypeptide that is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, pure. A substantially pure *sad* polypeptide may be obtained, for example, by extraction from a natural source (e.g., a bacterium), by expression of a recombinant nucleic acid encoding a *sad* polypeptide, or by chemically synthesizing the polypeptide. Purity can be measured by any appropriate method, e.g., by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

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A protein is substantially free of naturally associated components when it is separated from those contaminants that accompany it in its natural state. Thus, a protein that is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will be

5 substantially free from its naturally associated components. Accordingly, substantially pure polypeptides are not only those derived from the organisms in which they naturally occur, but also those synthesized in organisms genetically engineered to express a given polypeptide.

By "substantially pure DNA" is meant DNA that is free of the genes

10 which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA

15 or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA that is part of a hybrid gene encoding additional polypeptide sequence.

By "transformation" is meant any method for introducing foreign molecules into a cell (e.g., a bacterial, yeast, fungal, algal, plant, or animal

20 cell). Lipofection, DEAE-dextran-mediated transfection, microinjection, protoplast fusion, calcium phosphate precipitation, transduction (e.g., bacteriophage, adenoviral or retroviral delivery), electroporation, and biolistic transformation are just a few of the methods known to those skilled in the art which may be used.

25 By "transformed cell" is meant a cell (or a descendent of a cell) into which a DNA molecule encoding a polypeptide of the invention has been introduced, by means of recombinant DNA techniques.

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By "promoter" is meant a minimal sequence sufficient to direct transcription. Also included in the invention are those promoter elements which are sufficient to render promoter-dependent gene expression controllable for cell type, developmental status, and nutrient status, or inducible by external signals or agents; such elements may be located in the 5' or 3' or internal regions of the native gene.

By "operably linked" is meant that a gene and one or more regulatory sequences are connected in such a way as to permit gene expression when the appropriate molecules (e.g., transcriptional activator proteins) are bound to the regulatory sequences.

By "detectably-labeled" is meant any means for marking and identifying the presence of a molecule, e.g., an oligonucleotide probe or primer, a gene or fragment thereof, a cDNA molecule, or an antibody. Methods for detectably-labeling a molecule are well known in the art and include, without limitation, radioactive labeling (e.g., with an isotope such as ^{32}P or ^{35}S) and nonradioactive labeling (e.g., chemiluminescent labeling, or fluorescent labeling, e.g., with fluorescein).

By "sample" is meant a specimen containing bacterial cells, cell lysates, cell extracts, or mixtures of partially- or fully purified molecules, such as polypeptides or nucleic acids. Samples may be purified or fractionated by methods known in the art, including, but not limited to, differential precipitation or centrifugation, column chromatography, and gel electrophoresis.

By "specifically binds" is meant that an antibody recognizes and binds a given *sad* polypeptide but that does not substantially recognize and bind other molecules in a sample, e.g., a biological sample, that naturally includes

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protein. Preferred samples include bacterial cells and cell lysates or cell extracts, including partially purified cell extracts.

By "expose" is meant to allow contact between an animal, cell (prokaryotic or eukaryotic), lysate or extract derived from a cell, or molecule
5 derived from a cell, and a test compound, nutrient (such as citrate), or ion (such as Fe^{2+} or Fe^{3+}).

By "test compound" is meant a chemical, be it naturally-occurring or artificially-derived, that is surveyed for its ability to modulate biofilm formation, by employing one of the assay methods described herein. Test
10 compounds may include, for example, peptides, polypeptides, synthesized organic molecules, naturally occurring organic molecules, nucleic acid molecules, and components thereof.

By "assaying" is meant analyzing the effect of a treatment or exposure, be it chemical or physical, administered to cells (e.g., bacterial cells)
15 that are capable of forming biofilms. The material being analyzed may be a cell, a lysate or extract derived from a cell, or a molecule derived from a cell. The analysis may be, for example, for the purpose of detecting altered gene expression, altered nucleic acid stability (e.g. mRNA stability), altered protein stability, altered protein levels, or altered protein biological activity. The
20 means for analyzing may include, for example, nucleic acid amplification techniques, reporter gene assays, antibody labeling, immunoprecipitation, enzymatic assays, measurement of the presence and/or function of physical structures such as flagella or pili (e.g., by motility assays such as swarming or twitching motility assays), measurement of biofilm formation, such as
25 measurement of crystal violet (CV) staining or cell attachment, as described herein, and by other techniques known in the art for conducting the analysis of the invention.

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By "modulating" is meant changing, either by decrease or increase.

By "a decrease" is meant a lowering in the level of: a) protein, e.g., measured by ELISA; b) reporter gene activity, e.g., measured by reporter gene assay, for example, lacZ/ β -galactosidase, green fluorescent protein, luciferase, etc.; c) mRNA levels, e.g., measured by PCR relative to an internal control, for example, a "housekeeping" gene product such as ribosomal RNA; d) biofilm formation, e.g., as measured by crystal violet staining or counting attached cells; e) enzymatic activity of a polypeptide involved in biofilm formation, e.g., enzymatic activity of ClpP; or f) measurement of flagella or pilus function, e.g., by motility assays. In all cases, the lowering is preferably by at least 30%, more preferably by at least 40%, and even more preferably by at least 100%.

By "an increase" is meant a rise in the level of: a) protein, e.g., measured by ELISA; b) reporter gene activity, e.g., measured by reporter gene assay, for example, lacZ/ β -galactosidase, green fluorescent protein, luciferase, etc.; c) mRNA levels, e.g., measured by PCR relative to an internal control, for example, a "housekeeping" gene product such as ribosomal RNA; d) biofilm formation, e.g., as measured by crystal violet staining or counting attached cells; e) enzymatic activity of a polypeptide involved in biofilm formation, e.g., enzymatic activity of ClpP; or f) measurement of flagella or pilus function, e.g., by motility assays. In all cases, the rise is preferably by at least 50%, more preferably by at least 80%, and even more preferably by at least 95%.

By "protein" or "polypeptide" or "polypeptide fragment" is meant any chain of more than two amino acids, regardless of post-translational modification (e.g., glycosylation or phosphorylation), constituting all or part of a naturally-occurring polypeptide or peptide, or constituting a non-naturally occurring polypeptide or peptide.

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By "consecutive" is meant that a series of nucleotides exists as an unbroken sequence, i.e., uninterrupted by other nucleotides.

Brief Description of the Drawings

Fig. 1 is a representation of a photograph showing a biofilm formed by wild-type *P. fluorescens* and a graph showing quantitation of biofilm formation over time.

Fig. 2 is a graph demonstrating that protein synthesis is required for biofilm formation by *P. fluorescens*.

Fig. 3 is a representation of a photograph showing that biofilms are not formed by *P. fluorescens sad* mutants.

Fig. 4 (A-D) is a series of graphs showing biofilm formation on various surfaces by wild-type *P. fluorescens* and *sad* mutants.

Fig. 5 is a graph showing restoration of biofilm formation in a *clpP* mutant complemented with *clpP*⁺ (wild-type *clpP*).

Fig. 6 is a representation of two phase-contrast photomicrographs showing restoration of biofilm formation in a *clpP* mutant complemented with *clpP*⁺ (wild-type *clpP*).

Fig. 7 is a graph showing nutrient-mediated rescue of the biofilm formation defect in *P. fluorescens sad* mutants.

Fig. 8 is a diagram depicting a genetic model for biofilm formation in *P. fluorescens*.

Fig. 9 is a series of *sad* gene identifier sequences.

Fig. 10 is a representation of a photograph showing that nutrients affect biofilm formation in *E. coli*.

Fig. 11 is a representation of a photograph showing biofilm formation by wild-type and mutant *E. coli* strains.

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Fig. 12 is a graph that shows quantification of biofilm formation in various *E. coli* strains.

Figs. 13A-13D are representation of photomicrographs showing biofilm formation by wild-type and mutant *E. coli* strains.

5 Fig. 14 is a graph showing inhibition of biofilm formation by α -methyl-D-mannoside.

Fig. 15 is a diagram showing a model for initiation of *E. coli* biofilm formation.

10 Fig. 16 is a representation of a photograph showing biofilm formation phenotypes in wild-type and mutant *P. aeruginosa* strains.

Fig. 17 is a representation of a photograph of a motility assay of wild-type and mutant *P. aeruginosa* strains.

Fig. 18 is a representation of a photograph of a twitching motility assay of wild-type and mutant *P. aeruginosa* strains.

15 Fig. 19 is a representation of a photomicrograph showing the edge morphology of wild-type and mutant *P. aeruginosa* colonies.

Fig. 20 is a representation of a series of phase-contrast photomicrographs showing a timecourse of biofilm formation by wild-type *P. aeruginosa*.

20 Fig. 21 is a representation of a series of phase-contrast photomicrographs showing biofilms formed by wild-type and mutant *P. aeruginosa* at 3 hours and 8 hours after biofilm initiation.

Figs. 22A-22I are representations of phase-contrast photomicrographs that show the role of twitching motility in biofilm formation
25 by wild-type *P. aeruginosa*.

Fig. 23 is a schematic diagram of a model for the role of flagella and type IV pili in biofilm formation by *P. aeruginosa*.

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Description of the Preferred Embodiments

To dissect the complex phenomenon of biofilm formation, we employed a genetic approach to identify genes required for the early stages of biofilm formation. We found that pili are essential for initial attachment to abiotic surfaces, and that flagella are necessary for biofilm spreading upon such surfaces. In addition, motility, but not chemotaxis, is crucial during the early biofilm formation. We observed that protein synthesis is necessary for initiation of biofilm formation; in contrast, we noted that high osmolarity inhibits biofilm formation.

Our genetic screen in *P. fluorescens* identified *sad* genes whose products are involved in flagellar synthesis and function, and a *sad* gene whose product displays sequence homology to the *E. coli* ClpP protein, a component of the Clp protease.

Our findings indicate the existence of at least two genetic pathways involved in biofilm formation, and suggest that cells, in response to environmental signals, can adopt multiple strategies for initiating cell-to-surface interactions.

Biofilm formation in *P. fluorescens*

The experiments described herein show that: (a) *P. fluorescens* can form biofilms on an abiotic surface under a range of growth conditions; (b) protein synthesis is required for the earliest events of biofilm formation, suggesting that biofilm formation is a regulated process in this organism; (c) one (or more) extra-cytoplasmic proteins plays a role in interactions with an abiotic surface, and that the surface-exposed protein(s) may constitute the adhesion that mediates direct cell-to-surface contact; and (d) the osmolarity of the medium can impact the ability of *P. fluorescens* to form biofilms.

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Mutants of *P. fluorescens* defective for the initiation of biofilm formation on an abiotic surface (PVC) were isolated and designated surface attachment defective (*sad*). In addition to defects in forming biofilms on PVC, the *sad* mutants were also unable to initiate biofilm formation on other hydrophobic and hydrophilic surfaces. These data suggest that mutants identified on a single surface (i.e., PVC) may have defects in attachment on a wide range of abiotic (and potentially biotic) surfaces.

The initial search for mutants defective in biofilm formation was performed on minimal medium supplemented with glucose and CAA. However, approximately half of the *sad* mutants could be rescued for their biofilm formation defects (including the non-motile strains and the *clpP* mutant; see below) by supplementing the minimal glucose/CAA medium with iron, or by growing the strains with minimal medium supplemented with citrate or glutamate as the sole source of carbon and energy.

Not all nutrients that promote biofilm formation in the wild-type strain restore the ability of *sad* mutants to form a biofilm. For example, malate and mannitol allow growth and formation of biofilms in the wild type strain to levels comparable to glutamate- or citrate- grown cells, but do not rescue the biofilm formation defect of any of the *sad* mutants.

At this point it is not clear why glutamate and citrate, but not malate and mannitol, have the ability to rescue the biofilm formation defect of a subset of the *sad* mutants. *P. fluorescens* is a plant root colonizer, and it is possible that glutamate and/or citrate released by the plants may promote the formation of biofilms on the plant root. Consistent with this idea, recent studies have shown that citrate is the major organic acid found in exudates of roots and seedlings of tomato plants.

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Iron was also found to rescue a subset of the biofilm formation mutants. In these experiments, iron was provided at 3 μ M, a concentration of iron not normally seen in natural settings. Providing even 10-fold less iron in the medium (0.3 μ M) results in loss of the rescue of the biofilm formation phenotype.

Rescue of some *sad* mutants by growth on citrate, glutamate, or in the presence of exogenous iron indicates that cells can form biofilms on an abiotic surface in the absence of flagella-mediated motility. As described below, flagella appear to play an important role in the ability of cells to form biofilms. However, in our system, under certain environmental conditions (i.e., cells grown on citrate, glutamate, or in the presence of excess exogenous iron) the flagellum appears dispensable for formation of *P. fluorescens* biofilms on PVC. It is possible that the cells use an alternative form of locomotion in the absence of a flagellum, such as twitching motility, but only do so in response to the appropriate environmental signals.

Our biofilm mutants strains contain disruptions in novel genes, genes involved in flagellar synthesis, and in a gene that shows sequence homology to the *E. coli* ClpP protein. This protein is a subunit of the *E. coli* cytoplasmic Clp protease (Gottesman, S. and Maurizi, M.R., 1992, *Microbiol. Rev.* 56: 592-621). Clp protease is involved in the degradation of misfolded proteins, RpoS, IO protein, and Mu vir repressor (Chung, C. H., et al., 1996, *Biol. Chem.* 377: 549-554; Damerau, K. and St. John, A.C., 1993, *J. Bacteriol.* 175: 53-63; Pratt, L. and Silhavy, T. J., 1996, *Proc. Natl. Acad. Sci. USA* 93: 2488-2492; Schweder, T., et al., 1996, *J. Bacteriol.* 178: 470-476).

Based on its known activities and on our results, it appears that ClpP is involved in the regulation of biofilm formation. The target protein(s) of ClpP required for the regulation of biofilm formation (as well as the signaling

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pathway regulating Clp protease function) remain to be elucidated.

Interestingly, ClpP does not appear to be required for biofilm formation under all growth conditions. The *clpP* mutant was first isolated in a screen for strains defective in biofilm formation in minimal glucose/CAA medium. However,

- 5 ClpP function can be bypassed by growth on citrate, glutamate, or in the presence of exogenous iron.

We have found at least three overlapping pathways leading to the initiation of biofilm formation on an abiotic surface. One pathway (represented by 15 mutants) is functional on glucose/CAA medium independent of growth
10 with citrate, glutamate, or exogenous iron. A second pathway, represented by *sad-19*, appears to be utilized by cells grown on minimal glucose/CAA, minimal glucose/CAA plus iron, and minimal glutamate, however, the defect in the strain carrying *sad-19* can be bypassed by growth on citrate. Twelve mutants, represented by the strain carrying allele *sad-18*, are not rescued for
15 biofilm formation under any condition tested. These mutants may be defective for functions common to all of the biofilm formation pathways. The extent of the overlap among these pathways is unclear and will require further analyses. It is also possible that there are additional, as yet unidentified signals, which regulate biofilm formation.

- 20 Fig. 8 shows our current genetic model for the initiation of biofilm formation in *P. fluorescens*. We propose that multiple pathways can be utilized to initiate interactions with a surface, and that these pathways can be regulated by varying environmental parameters. Environmental signals may include carbon/energy sources and iron availability. Our genetic analyses indicate that
25 there may be functions, such as those disrupted in the strain carrying allele *sad-18*, which are common to all known biofilm formation pathways. All of the mutants shown here, except for *fliP*, *flaE*, *sad-16*, *sad-20*, and *sad-22* are

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motile. Our genetic analysis has begun to decipher the signaling pathways and structural genes which play a role in forming biofilms on an abiotic surface. It is still unclear which loci are required for sensing and responding to the signals required for biofilm formation (ClpP may play a role in this process) and which
5 loci participate directly in the cell-to-surface interactions.

Of the 24 *P. fluorescens* mutants analyzed in this study and shown in Fig. 8, only 3 of the mutants had defects in genes of known function. These data suggest that we have isolated a number of new genes. Based on our molecular analyses of the DNA sequence flanking the transposon insertions, we
10 know that the mutants are not siblings. However, it is possible that we have identified multiple mutations within a single gene or operon, a question that is currently under investigation.

Biofilm formation in *E. coli*

In addition to using *P. fluorescens* as an experimental model, we
15 have used the well-studied and genetically tractable organism, *E. coli*, to rapidly identify genes required for the initial stages of biofilm formation.

As a result of our studies, we have made the surprising discovery that, under the conditions used in our experiments, chemotaxis is not required for the initiation of *E. coli* biofilm formation. In contrast, we conclude that
20 motility is critical for normal biofilm formation; cells defective in flagellar biosynthesis or motility attach poorly to PVC, and the few cells that do attach are often located in small, dense clusters. The observation of small cell clusters in paralyzed or non-flagellated cell strains suggests that, in addition to enhancing initial surface contact, motility contributes to the initial spread of a
25 biofilm by facilitating movement of cells along an abiotic surface.

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Although it is possible that flagella also play a role in mediating actual adherence to abiotic surfaces, the fact that there is no phenotypic difference observed in the attachment (at the microscopic level) of paralyzed cells and non-flagellated cells to surfaces, compared to flagellated cells, does not support this hypothesis. Although flagella, motility, and/or chemotaxis have previously been implicated in biofilm formation in other organisms (DeFlaun, et al., *Appl. Environ. Microbiol.* 60:2637-2642, 1994; Graf, et al., *J. Bacteriol.*, 176:6986-6991, 1994; Korber, et al., *Appl. Environ. Microbiol.*, 60:1421-1429, 1994; Korber et al., *Pseudomonas fluorescens Microb. Ecol.*, 18:1-19, 1989; Lawrence, et al., *Microb. Ecol.*, 14:1-14, 1987; Mills and Powelson, *Bacterial Adhesion: Molecular and Ecological Diversity*, John Wiley & Sons, Inc., New York, Vol. pp. 25-57, 1996), these studies did not provide molecular characterization of the strains; therefore, the possibility that these strains contained pleiotropic defects could not be ruled out.

Moreover, prior to our molecular descriptions of the lesions conferring biofilm defects, it has been difficult to clearly define potential roles (adherence, motility, and/or chemotaxis) for flagella in biofilm development. For example, one could envision flagella functioning in three non-mutually exclusive roles: (1) flagellar-mediated chemotaxis might enable planktonic cells to swim towards nutrients associated with a surface or towards signals generated by cells attached to an abiotic surface, (2) flagellar-mediated motility might be required to overcome repulsive forces at a surface, enabling bacteria to initially reach a surface, and/or (3) flagella might function in a direct fashion by physically adhering to an abiotic surface.

Our studies show that, in contrast to flagella, type I pili are essential for initial attachment of *E. coli* prior to biofilm formation: cells harboring lesions in genes encoding proteins involved in the regulation or biogenesis of

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type I pili do not efficiently attach to the abiotic surfaces tested. Indeed, only rarely do cells lacking type I pili attach. Moreover, cells lacking pili never form clusters of adhered cells, as do paralyzed and non-flagellated cells that possess pili. In addition, we discovered that attachment is inhibited by the presence of mannose or α -methyl-D-mannose. Type I pili contain the mannose-specific adhesin, FimH, which plays a role in facilitating pathogenesis through specific interactions between FimH and mannose oligosaccharides present on eukaryotic cell surfaces. The observation that FimH is also critical for attachment to abiotic surfaces was surprising and leads us to assign a novel role to type I pili.

There are two simple models to explain how FimH functions to attach to abiotic surfaces. First, FimH may play an indirect role, binding to sugars and/or proteins associated with the abiotic surface. Although this is a formal possibility, this model would predict that small amounts of mannose might interact with the surface and function to stimulate attachment. However, the observation that even the smallest amount of mannose added inhibited attachment argues against this hypothesis. Alternatively, it is possible that the interaction is direct and involves a region of FimH involved in non-specific binding to abiotic surfaces. If this is the case, then the binding of mannose to FimH may somehow alter its conformation, masking the FimH region that interacts with abiotic surfaces.

The mannose-dependent inhibition of *E. coli* biofilm formation on abiotic surfaces may have general applications to other biofilm-forming bacteria. Bacteria that form biofilms on surfaces in medically and/or industrially relevant environments may also require the integrity of adhesions analogous to the requirement of *E. coli* for FimH. Thus, it is possible that the

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formation of problematic biofilms could be blocked through treatment with innocuous materials such as mannose.

The observations described here lead to the following model to describe the initiation of *E. coli* biofilm formation. Motility, but not chemotaxis, enhances cells' initial contact with an abiotic surface. This requirement may reflect a necessity to overcome repulsive forces present at an abiotic surface to be colonized. Once a surface is reached, type I pili are required to achieve stable cell-to-surface attachment. The presence of the FimH adhesion, when it is not bound to mannose, promotes such stable adherence to abiotic surfaces. Finally, we hypothesize that motility facilitates the development of a mature biofilm by allowing movement along a surface, thereby promoting spread of the biofilm.

In the work described herein, the alleles isolated affect factors required for flagellar biogenesis, motility, and the regulation and biogenesis of type I pili. It is well established that flagellar-mediated motility and the ability to produce a number of pili contribute to the virulence of pathogenic bacteria. This leaves us with the suggestive overlap of functions essential for both biofilm formation and functions needed for pathogenicity. In this regard, screens such as the one described here may prove useful in the identification of gene products important for the pathogenicity of a variety of bacteria. In addition, the work with *E. coli* may serve as a paradigm for the study of bacteria less amenable to genetic and molecular approaches. Although we predict extensive similarities in the molecular mechanisms utilized by other biofilm-forming bacteria, distinguishing details will no doubt arise. Such distinctions should be especially informative as to the particular mechanisms utilized by bacteria that live in various environmental niches.

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Biofilm formation in *P. aeruginosa*

We have isolated a non-motile strain of *P. aeruginosa* (containing an insertion mutation in a *flgK* homolog) that is unable to form a biofilm. This finding shows that flagella, motility, and/or chemotaxis are required for *P.*

5 *aeruginosa* biofilm development. It is noteworthy that the *flgK* mutant of *P. aeruginosa* displays a phenotype that differs from the *E. coli* flagellar mutants. Specifically, the *flgK* *P. aeruginosa* strain has only a few cells that attach to PVC and no micro-colonies are formed. This highlights the point that despite a clear conservation (between *E. coli* and *P. aeruginosa*) in the use of flagella
10 during biofilm development, the aspect(s) of flagellar structure and function utilized appear to be different.

In addition, we have found insertion mutations in genes required for functional type IV pili, which interfere with normal *P. aeruginosa* biofilm formation. *P. aeruginosa* strains lacking type IV pili form monolayers of cells
15 attached to PVC, but do not proceed past this stage, i.e., do not form micro-colonies or multi-layered biofilms.

The above findings suggest that similar surface structures, such as pili and flagella, are important in both *E. coli* and *P. aeruginosa* for normal biofilm development. However, the precise functions of these structures,
20 although perhaps overlapping, are not completely conserved between these species.

Screens for compounds that affect biofilm formation

Compounds that modulate biofilm formation have various medical, industrial, agricultural, and public works uses. For example, compounds that
25 stimulate biofilm formation could be used to improve colonization of plant roots by beneficial bacteria. Conversely, compounds that inhibit biofilm

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formation could be employed to restrict growth of bacteria on contact lenses, medical implants (e.g., artificial hips), walls of catheters, water and sewerage pipes, and within the lungs of infected patients.

The invention provides screens for the isolation of such useful
5 biofilm-modulating compounds. For instance, the biofilm formation assays described in Examples I-IV below may be used to measure the effect of test compounds on biofilm formation, relative to biofilm formation in untreated control samples. High-throughput screens may also be readily performed.

Furthermore, the effect of test compounds on biofilm formation may
10 be indirectly assessed by measuring their effect on *sad* biological activity (e.g., transcription of a *sad* gene or *sad*/reporter gene; post-transcriptional degradation or translation of a *sad* mRNA or *sad*/reporter mRNA; or post-translational degradation, enzymatic function, or structural function of a *sad* polypeptide or *sad*/reporter polypeptide) in treated vs. untreated samples, using
15 enzymatic, ELISA, PCR, and reporter gene assays described herein and/or known in the art.

The effect of test compounds on biofilm formation may also be assessed by measuring their influence on pilus or flagellum synthesis, structure, or function, e.g., using ELISA, PCR, and reporter gene assays, or the various
20 motility assays described below, all of which are well known to skilled artisans.

a) ELISA for the detection of compounds that modulate biofilm formation

Enzyme-linked immunosorbant assays (ELISAs) are easily incorporated into high-throughput screens designed to test large numbers of
25 compounds for their ability to modulate levels of a given protein. When used in the methods of the invention, changes in the level of a *sad* protein in a sample,

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relative to a control, reflect changes in the biofilm formation status of the cells within the sample. Protocols for ELISA may be found, for example, in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1997. Samples, such as lysates from bacterial cells treated

5 with potential biofilm formation modulators, are prepared (see, for example, Ausubel et al., *supra*), and are loaded onto the wells of microtiter plates coated with "capture" antibodies against one of the *sad* proteins. Unbound antigen is washed out, and a *sad* protein-specific antibody, coupled to an agent to allow for detection, is added. Agents allowing detection include alkaline phosphatase

10 (which can be detected following addition of colorimetric substrates such as *p*-nitrophenolphosphate), horseradish peroxidase (which can be detected by chemiluminescent substrates such as ECL, commercially available from Amersham, Malvern, PA) or fluorescent compounds, such as FITC (which can be detected by fluorescence polarization or time-resolved fluorescence). The

15 amount of antibody binding, and hence the level of a *sad* protein within a lysate sample, is easily quantitated on a microtiter plate reader.

As a baseline control for *sad* protein levels in untreated cells, a sample from untreated cells is included. Ribosomal proteins may be used as internal standards for absolute protein levels, since their levels do not change

20 over the preferred timecourse (e.g., 0 to 10 hours for a standard biofilm assay, or 0 to 30 minutes for a rapid biofilm assay, as described in the examples below). Alternatively, bacteria or bacterial cell lysate may be directly exposed to a compound in the absence of biofilm assay conditions. A positive assay result, for example, identification of a compound that decreases biofilm

25 formation, is indicated by a decrease in *sad* protein levels, relative to *sad* protein levels observed in untreated cells that are allowed to form a biofilm.

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Conversely, an increase in *sad* protein levels, relative to *sad* protein levels in untreated cells, indicates a compound that increases biofilm formation.

b) Reporter gene assays for compounds that modulate biofilm formation

Assays employing the detection of reporter gene products are extremely sensitive and readily amenable to automation, hence making them ideal for the design of high-throughput screens. Assays for reporter genes may employ, for example, colorimetric, chemiluminescent, or fluorometric detection of reporter gene products. Many varieties of plasmid and viral vectors containing reporter gene cassettes are easily obtained. Such vectors contain cassettes encoding reporter genes such as *lacZ*/ β -galactosidase, green fluorescent protein, and luciferase, among others. We have constructed strains containing *sad* mutations described herein with *lacZ* fusions that may be used in such screens. Cloned DNA fragments encoding transcriptional control regions of interest are easily inserted, by DNA subcloning, into such reporter vectors, thereby placing a vector-encoded reporter gene under the transcriptional control of any gene promoter of interest. The transcriptional activity of a *sad* gene promoter operably linked to a reporter gene can then be directly observed and quantitated as a function of reporter gene activity in a reporter gene assay.

Bacteria containing one or more *sad*/reporter gene constructs are cultured under the appropriate conditions, e.g., under conditions that promote biofilm formation in a screen for a compound that inhibits biofilm formation. Alternatively, bacteria or bacterial cell lysates may be directly exposed to a compound in the absence of biofilm assay conditions. Compounds to be tested for their effect on biofilm formation are added to the bacteria. At appropriate timepoints, bacteria are lysed and subjected to the appropriate reporter assays,

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for example, a colorimetric or chemiluminescent enzymatic assay for lacZ/ β -galactosidase activity, or fluorescent detection of GFP. Changes in reporter gene activity of samples treated with test compounds, relative to reporter gene activity of appropriate untreated control samples indicate the presence of a compound that modulates biofilm formation.

In one embodiment, one construct could comprise a reporter gene such as lacZ or chloramphenicol acetyltransferase (CAT), operatively linked to a promoter from a *sad* gene. *Sad*/reporter gene constructs may be present within the genomic DNA of a bacterial cell to be tested, or may be present as an episomal DNA molecule, such as a plasmid. A second reporter gene operably linked to a second promoter is included as an internal control. This could be an episomal reporter gene operatively linked, for example, to a glucose phosphotransferase or phosphofructokinase gene. The glucose phosphotransferase or phosphofructokinase gene is expressed in bacteria growing on glucose. The amount of activity resulting from an internal control reporter gene that is operably linked to a glucose kinase (or analogous) promoter will indicate the proportion of live growing cells within a treated sample, relative to an untreated sample. The *sad* reporter gene activity is normalized to the internal control reporter gene activity. As a result of the normalization, a relative decrease in *sad* promoter activity indicates a compound that modulates biofilm formation by down-regulating *sad* gene transcription (rather than, e.g., a compound that inhibits cell growth or kills cells, thus giving the appearance of decreased *sad* gene transcription).

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c) *Quantitative PCR of sad mRNA as an assay for compounds that modulate biofilm formation*

The polymerase chain reaction (PCR), when coupled to a preceding reverse transcription step (rtPCR), is a commonly used method for detecting vanishingly small quantities of a target mRNA. When performed within the linear range, with an appropriate internal control target (employing, for example, a housekeeping gene such as the glucose phosphotransferase or phosphofructokinase), such quantitative PCR provides an extremely precise and sensitive means for detecting slight modulations in mRNA levels. Moreover, this assay is easily performed in a 96-well format, and hence is easily incorporated into a high-throughput screening assay. Bacterial cells are cultured under the appropriate biofilm-inducing or -inhibiting conditions, in the presence or absence of test compounds. The cells are then lysed, the mRNA is reverse-transcribed, and the PCR is performed according to commonly used methods (such as those described in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1997), using oligonucleotide primers that specifically hybridize with the nucleic acid of interest. In one embodiment, the target mRNA could be that of one or more of the *sad* genes. Analogously to the *sad* protein result described above, changes in product levels of samples exposed to test compounds, relative to control samples, indicate test compounds with biofilm formation-modulating activity.

d) *Test Compounds*

In general, novel compounds for modulating biofilm formation are identified from large libraries of both natural product or synthetic (or semi-synthetic) extracts or chemical libraries according to methods known in the art. Those skilled in the field of chemical discovery and development will

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understand that the precise source of test extracts or compounds is not critical to the screening procedure(s) of the invention. Accordingly, virtually any number of chemical extracts or compounds can be screened using the exemplary methods described herein. Examples of such extracts or compounds include, but are not limited to, plant-, fungal-, prokaryotic- or animal-based extracts, fermentation broths, and synthetic compounds, as well as modification of existing compounds. Numerous methods are also available for generating random or directed synthesis (e.g., semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, and nucleic acid-based compounds. Synthetic compound libraries are commercially available from Brandon Associates (Merrimack, NH) and Aldrich Chemical (Milwaukee, WI). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant, and animal extracts are commercially available from a number of sources, including Biotics (Sussex, UK), Xenova (Slough, UK), Harbor Branch Oceanographics Institute (Ft. Pierce, FL), and PharmaMar, U.S.A. (Cambridge, MA). In addition, natural and synthetically produced libraries are produced, if desired, according to methods known in the art, e.g., by standard extraction and fractionation methods. Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

In addition, those skilled in the art of chemical discovery and development readily understand that methods for dereplication (e.g., taxonomic dereplication, biological dereplication, and chemical dereplication, or any combination thereof) or the elimination of replicates or repeats of materials already known for their effects on biofilm formation should be employed whenever possible.

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When a crude extract is found to modulate biofilm formation, further fractionation of the positive lead extract is necessary to isolate chemical constituents responsible for the observed effect. Thus, the goal of the extraction, fractionation, and purification process is the careful characterization and identification of a chemical entity within the crude extract having an effect on biofilm formation. The same assays described herein for the detection of activities in mixtures of compounds can be used to purify the active component and to test derivatives thereof. Methods of fractionation and purification of such heterogenous extracts are known in the art. If desired, compounds shown to be useful agents for treatment are chemically modified according to methods known in the art. Compounds identified as being of medical or industrial value may be subsequently analyzed using the appropriate biofilm formation model.

Below are examples of high-throughput systems useful for evaluating the efficacy of a molecule or compound in stimulating or inhibiting biofilm formation.

e) Uses

Compounds identified using any of the methods disclosed herein may be administered to patients or experimental animals, applied to the fluid-contacting surfaces of medical devices, such as catheter lines, contact lenses, and surgical implants, applied to the fluid-contacting surfaces of industrial devices, such as pipes, or applied to soil, seeds, or plant roots by methods known in the various medical, manufacturing, and agricultural arts. Moreover, fluid-contacting surfaces may be impregnated with the compounds of the invention.

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The following examples are meant to illustrate, not limit, the invention.

Example I: General Methods

Bacterial strains, media, and chemicals.

5 All *P. fluorescens* strains and plasmids used in the experiments described in Example II below are shown in Table 1. *P. fluorescens* strain WCS365 and *P. aeruginosa* strain PA14 were grown at 30°C and 37°C, respectively, on rich medium (Luria Bertani; LB) or minimal medium, unless otherwise noted. The minimal medium used was M63 (Pardee, A.B., et al.,
10 1959, *J. Mol. Biol.* 1: 165-178) supplemented with glucose (0.2%), MgSO₄ (1 mM) and, where indicated, casamino acids (CAA, 0.5%), citric acid (0.4%), glutamic acid (monosodium salt, 0.4%) or FeSO₄·7H₂O (3 µM). Unless otherwise indicated, all carbon sources were provided at 0.4%.

For the experiments described in Example III, W3110 (*E. coli* K12
15 F-1- IN(rmD-rmE)1 rph-1) was used as the parental strain; all strains described in Example III are either W3110 or derivatives of this strain. The media and growth conditions used have been previously described (Pardee, A.B. et al., *supra*; Silhavy, T. et al., *Experiments with gene fusions*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1984), and casamino acids were added at
20 a concentration of 0.5%.

Whenever antibiotics were used, they were added at the following concentrations: *E. coli* : ampicillin (Ap), 150 µg/ml; naladixic acid (Nal), 20 µg/ml; tetracycline (Tc), 15 µg/ml; kanamycin (Kn), 50 µg/ml; *P. fluorescens*: Tc, 150 µg/ml; gentamycin (Gm), 100 µg/ml; Kn, 500 µg/ml; *P. aeruginosa*:
25 Tc, 150 µg/ml. Pronase E was obtained from Sigma Chemical Co. (St. Louis, MO).

Table 1. Strains and Plasmids

Strain (Relevant genotype)	Reference
<i>Pseudomonas fluorescens</i> strain WCS365	(Geels and Schippers, <i>Phytopathol. Z.</i> , 108 :207-214, 1983); Simons, et al., <i>Mol.</i> <i>Plant Microbe Inter.</i> , 9 :600-607, 1996)
5	
<i>P. fluorescens</i> <i>clpP</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>fliP</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>flaE</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>sad-10</i> ::Tn5-B30(Tc ^r)	This study
10	
<i>P. fluorescens</i> <i>sad-16</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>sad-18</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>sad-19</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>sad-20</i> ::Tn5-B30(Tc ^r)	This study
<i>P. fluorescens</i> <i>sad-21</i> ::Tn5-B30(Tc ^r)	This study
15	
<i>P. fluorescens</i> <i>sad-22</i> ::Tn5-B30(Tc ^r)	This study
ZK126 (<i>clpP</i> ⁺ , <i>E. coli</i> W3110)	(Connell, et al., <i>Mol. Microbiol.</i> , 1 :195-204, 1987)
Plasmids	
pTn5-B22 (Gm ^r , <i>lacZ</i>)	(Simon, et al., <i>Gene</i> , 80 :160-169, 1989)
20	
pTn5-B30 (Tc ^r)	(Simon, et al., <i>Gene</i> , 80 :160-169, 1989)
pUC181.8 (Ap ^r)	(Frank, et al., <i>J. Bacteriol.</i> , 178 :5304-5313, 1989)
pSU39 (Kn ^r)	(Martinez, et al., <i>Gene</i> , 68 :159-162, 1988)
pSMC26 (<i>clpP</i> ⁺ , Kn ^r , derivative of pSMC28)	This study
25	
pSMC28 (derivative of pSU39, Kn ^r , stably maintained in <i>Pseudomonas</i> spp.)	This study

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Molecular and genetic techniques.

All plasmids were constructed in *E. coli* JM109 using standard protocols (Ausubel, F.A. et al., 1990, Current Protocols in Molecular Biology, Wiley Interscience, NY) then transferred to the appropriate strains by electroporation (Bloemberg, G.V. et al., 1997, *Appl. Environ. Microbiol.*, 63, 4543-4551)).

a) Transduction and transposon mutagenesis

Generalized transduction in *E. coli* using P1 vir was performed as previously described (Silhavy, et al., *supra*). Genetic linkage analysis in *E. coli* was performed by using a P1 vir lysate that had been grown on a pool of cells containing transposons randomly inserted throughout the chromosome (Kleckner, N., et al., 1991, *Methods in Enzymology*, 204, 139-180).

Transductions into *P. aeruginosa* were performed as reported (Jensen, E.C. et al., 1998, *Appl. Environ. Microbiol.*, 64, 575-580).

Transposon mutants in *P. fluorescens* were generated using a modification of published protocols (Simons, M., et al., 1996, *Mol. Plant Microbe Inter.* 9: 600-607). Recipient (*P. fluorescens*) and donor (*E. coli* S17-1/pTn5::B30(Tc) or *E. coli* S17-1/pTn5::B322(Gm)) were grown in LB to late log phase ($A_{600} = 0.6-0.8$). After incubating *P. fluorescens* at 42°C for 15 min, 1 mL of the recipient was added to 0.25 mL of the donor in a 1.5 mL Eppendorf tube. The cells were pelleted in a microfuge, the medium decanted, and the cells resuspended in 50 µL of LB, and the entire 50 µL was spotted on an LB plate and incubated at 30°C for 24-48 hrs. After incubation, the cells were scraped from the LB plate and resuspended in 1 mL LB and 250 µL was subsequently plated on LB plates supplemented with Tc or Gm (to select for the Tn5 mutants) and Nal (to select against growth of the *E. coli* donor). The

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resulting transposon mutants were screened for biofilm formation as described below.

Transposon mutants in *P. aeruginosa* were generated with Tn5-B30(Tcr) using a modification of published protocols (Simon, R., 1989, *Gene*, 80, 160-169) The resulting transposon mutants were screened for biofilm formation as described below.

b) PCR

The DNA sequence flanking transposon mutants was determined using arbitrary PCR (Caetano-Annoles, G., 1993, *PCR Methods Appl.* 3: 85-92). In this technique, the DNA flanking insertion sites is enriched in two rounds of amplification using primers specific to the ends of the Tn5 element and primers to random sequence that anneal to chromosomal sequences flanking the transposon.

PCR of P. fluorescens and P. aeruginosa transposon mutant DNA

In the first round, a primer unique to the right end of Tn5 elements (Tn5Ext, 5'-GAACGTTACCATGTAGGAGGTC-3'; SEQ ID NO: 25) and arbitrary primer #1 (ARB1, 5'-GGCCACGCGTCGACTAGTACNNNNNNNNNNGATAT-3'; SEQ ID NO: 26) were used in 100 uL PCR reactions (1X Vent Polymerase buffer, MgSO₄ (1mM), dNTPs (0.25 mM), and Vent, exo-DNA polymerase (2 U) with 5 mL of an overnight LB-grown culture as the source of DNA. The first round reaction conditions were: i), 5 min. at 95°C ii) 6X (30 sec at 95°C, 30 sec at 30°C, 1 min 30 sec at 72°C), iii) 30X (30 sec at 95°C, 30 sec at 45°C, 2 min at 72°C).

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Reactions for the second round of PCR were performed as described for the first round, except 5 μ L of the first round PCR product was used as the source of DNA and the primers were ARB2 (5'-GGCCACGCGTCGACTAGTAC-3'; SEQ ID NO: 27) and Tn5Int (5'-CGGGAAAGGTTCCGTTTCAGGACGC-3'; SEQ ID NO: 28). The ARB2 sequence is identical to the 5'-end of the ARB1 primer and the sequence of Tn5Int is identical to the right-most end of Tn5, near the junction between the transposon and the chromosome. The reaction conditions for the second round were 30X (30 sec at 95°C, 30 sec at 45°C, 2 min at 72°C).

10 PCR products were purified either from an agarose gel using β -agarase (NEB, Beverly, MA) or with the QIAquick Spin PCR Purification Kit (Qiagen Inc, Chatsworth, CA) as described by the manufacturer without modification. PCR products were sequenced using the Tn5Int primer at the Micro Core Facility, Department of Microbiology and Molecular Genetics,
15 Harvard Medical School and compared to the Genbank DNA sequence database using the BLASTX program (Altschul, S.F., et al., 1990. *J. Mol. Biol.* 215: 403-410).

PCR of E. coli transposon mutant DNA

The first round of PCR reactions used the following primers: ARB1
20 (GGCCACGCGTCGACTAGTACNNNNNNNNNNNGATAT; SEQ ID NO: 26) or ARB6 (GGCCACGCGTCGACTAGTACNNNNNNNNNNNACGCC; SEQ ID NO: 29) and OUT1-L (CAGGCTCTCCCGTGGAG; SEQ ID NO: 30). The second round of PCR reactions used the following primers: ARB2 (GGCCACGCGTCGACTAGTAC; SEQ ID NO: 27) and PRIMER1L
25 (CTGCCTCCCAGAGCCTG; SEQ ID NO: 31).

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Following the second round of PCR amplification, PCR products were separated a 1.0% low melt agarose gels, and bands were excised from the gel. The agarose was digested with β -agarase, and the DNA was subjected to DNA sequence analysis utilizing PRIMER1L. Sequence analysis was carried out at the Biopolymers Laboratory of the Department of Biological Chemistry and Molecular Pharmacology of Harvard Medical School.

c) Southern blots

Southern blots were performed as follows: chromosomal DNA of the *sad* mutants was prepared (Pitcher, D.G., 1989, *Lett. Appl. Microbiol.*, 8, 151-156.), digested with *EcoRI* (Tn5-B30 does not have a *EcoRI* site), and transferred to GeneScreen Plus (NEN Research Products, Boston, MA) as reported (Ausubel, F.A. et al., 1990, *Current Protocols in Molecular Biology*. Wiley Interscience, NY). The hybridization was performed with the ECL direct nucleic acid labeling and detection system (Amersham Life Science, Buckinghamshire, England) following the manufacturer's instructions without modification. The DNA probe used was derived from the insertion sequence element (IS50) of Tn5 and generated using PCR with the Tn5 element as a template. The PCR primers used to generate the probe were IS50R.1 (5'-GCTTCCTTTAGCAGCCCTTGCGC-3'; SEQ ID NO: 32) and IS50R.2 (5'-CTTCCATGTGACCTCCTAACATGG-3'; SEQ ID NO: 33).

d) Cloning of integrated transposons

Selected transposons were cloned to determine additional DNA sequence flanking the transposon. Chromosomal DNA was prepared (Pitcher, D.G., et al., 1989, *Lett. Appl. Microbiol.*, 8: 151-156), digested with *EcoRI* (there are no *EcoRI* sites in these Tn5 derivatives), and ligated with

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pBluescript, KS⁺, Ap^r (Stratagene, La Jolla, CA) previously digested with *Eco*RI. Ligation mixes were electroporated into *E. coli* JM109, plated on LB supplemented with Ap, then printed onto LB supplemented with Ap (150 µg/ml) and Tc (10 µg/ml). The Ap^rTc^r colonies were purified, plasmid DNA prepared, and the plasmids were sequenced with the Tn5Ext primer.

e) Construction of the *clpP*-carrying plasmid

A derivative of pSU39 (Martinez, E., et al., 1988, *Gene* 68: 159-162) was constructed that is stably maintained in *Pseudomonas* spp. The 1.8 kb *Pst*I "stabilizing fragment" of pUC181.8 (Frank, D.W., 1989, *J. Bacteriol.* 171: 5304-5313) was cloned into the *Pst*I site of pSU39, generating the plasmid pSMC28. The stabilizing fragment allows the stable replication of plasmids in *Pseudomonas* spp. To generate the plasmid required for complementation analysis, the *clpP* gene of *E. coli* (ZK126 W3110) was amplified with primers flanking *clpP* and also including the predicted promoter region of this gene. The PCR product was cloned into pSMC28, previously digested with *Hinc*II, generating plasmid pSMC26 (*clpP*⁺).

Motility Assays.

Following strain construction involving alleles that affect flagella, motility, and/or chemotaxis, the presence (or absence) of flagella was confirmed using a simple staining procedure that has been previously described (Heimbrook, et al., 1989, *J. Clin. Microbiol.*, 27, 2612-2615). Motility and chemotaxis were analyzed using both swarm assays (Adler, J., 1966, *Science*, 153, 708-716.; Wolfe, A.J. and Berg, H.C., 1989, *Proc. Natl. Acad. Sci. USA*, 86, 6973-6977) and phase contrast microscopy of living cells. INK1324 was used for insertion mutagenesis of W3110 as previously described (Kleckner, et

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al., *supra*). Motility assays were performed on minimal agar plates (0.3%) supplemented with glucose and CAA and the distance that the cells migrated through the agar was determined after 16-24 hrs. Twitching motility was assessed as described (Whitchurch, C.B. et al., 1990, *Gene*, 101, 33-44).

5 **Biofilm formation assay.**

Our standard biofilm formation assay involves starting with relatively low number of cells ($\sim 10^6$ CFU/ml) in minimal M63 medium supplemented with glucose and casamino acids (CAA) at 25°C to 37°C for 8 to 48 hours. Biofilm development can be monitored indirectly by following the increase in crystal violet (CV) staining over time; this purple dye stains the bacterial cells, but does not stain plastics such as polyvinylchloride (PVC). Alternatively, biofilm formation can be monitored with a rapid assay by starting with $\sim 10^8$ CFU/ml. In this way, biofilm formation can be detected after just 30 min. Using these assays, we tested the impact of various growth conditions and environmental signals on biofilm formation and searched for mutants defective in this process.

a) Screen for mutants defective in biofilm formation

This assay is based on the ability of bacteria to form biofilms on polyvinylchloride plastic (PVC), a material which is used to make catheter lines (Lopez-Lopez, G., et al., 1991, *J. Med. Microbiol.* 34: 349-353). Biofilm formation was assayed by the ability of cells to adhere to the wells of 96-well microtiter dishes made of PVC (Falcon 3911 Microtest III Flexible Assay Plate, Becton Dickinson Labware, Oxnard, CA) using a modification of a reported protocol (Fletcher, M., 1977, *Can. J. Microbiol.* 23: 1-6). The indicated medium (100 μ L/well) was inoculated either from cells patched on LB agar

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plates using a multi-prong device or a 1:100 dilution from an overnight LB culture. After inoculation, plates were incubated at 25°C to 37°C for 8-48 hours for *P. fluorescens* and *P. aeruginosa* or 10-24 hours for *E. coli*, then 25 µL of a 1% solution of CV was added to each well (this dye stains the cells, but not the PVC), the plates were incubated at room temperature for ~15 min, rinsed thoroughly and repeatedly with water, and scored for the formation of a biofilm. Fig. 1 shows the formation of the biofilm at the air-medium interface, monitored over a 10 hr period. Because of the growth conditions used in this assay (oxygen is the primary electron acceptor) *P. fluorescens* grows predominantly near the surface of medium in the microtiter wells. Crystal-violet-stained, surface-attached cells were quantified by solubilizing the dye in ethanol and determining the absorbance at 600 nm. The A₆₀₀ values increased with time up to about 8-10 hours of incubation. Wells developed at 0 and 10 hours are shown above the graph in Fig. 1.

15 b) Rapid biofilm formation assay

To assess the formation of biofilms after 30 min instead of 10 hrs, *P. fluorescens* was grown overnight under conditions that only weakly stimulate biofilm formation (minimal glucose medium) resulting in a viable count of ~10⁸ colony forming units (CFU)/ml. The planktonic cells were centrifuged, and resuspended in an equal volume of fresh minimal medium supplemented with glucose and CAA (conditions that stimulate biofilm formation) and assessed for biofilm formation using the CV-based assay described above. This method was used to assess the effects of the protein synthesis inhibitor Tc and protease treatment on biofilm formation.

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c) Quantitation of biofilm formation

Biofilm formation was quantified by the addition of 2 X 200 μ L of 95% ethanol to each CV-stained microtiter dish well, the ethanol was transferred to a 1.5 ml Eppendorf tube, the volume brought to 1 mL with dH₂O, and the absorbance determined at 540 nm in a spectrophotometer (DU-640 Spectrophotometer, Beckman Instruments Inc., Fullerton, CA). Alternatively, CV-stained biofilms were solubilized in 200 μ L of 95% ethanol, of which 125 μ L was transferred to a new polystyrene microtiter dish (Costar Corporation, Cambridge, MA), and the absorbance determined with a plate reader at 600 nm (Series 700, Microplate Reader, Cambridge Technology, Inc., Cambridge, MA). We also used these methods to quantify biofilm formation on polystyrene (Pro-bind Assay Plate, non-tissue culture treated, Becton Dickson & Co., Lincoln Park, NJ), polypropylene (1.5 mL microcentrifuge tube, Marsh Biomedical Products, Inc., Rochester, NY), and borosilicate glass (Kimax 51 culture tubes, VWR, S. Plainfield, NJ).

d) Microscopy

The visualization of *P. fluorescens* cells attached to PVC was performed as reported (Bloemberg, G.V., et al., 1997, *Microbiol.* 63: 4543-4551). Visualization of *P. aeruginosa* cells attached to PVC was performed by phase contrast microscopy (400X magnification) using a Nikon Diaphot 200 inverted microscope (Nikon Corp., Tokyo, Japan). The images were captured with a black and white CCD72 camera integrated with a Power Macintosh 8600/300 computer with video capability (Macintosh, Cupertino, CA). The images were processed with Scion Image software, a modification of NIH Image (NIH, Washington, DC) by the Scion Corporation (Frederick, MD).

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e) Quantification of CV-stained attached *P. aeruginosa* cells and growth curves

Attached cells were quantified as described previously, with a few modifications (Genevaux, et al., 1996, *FEMS Microbiol. Lett.*, 142, 27-30; O'Toole, G.A. and Kolter, R., 1998, *Mol. Microbiol.*, 28:449-461). After wells
5 had been stained with 125 μ l of 1.0% CV, rinsed, and thoroughly dried, the CV was solubilized by the addition of 200 μ L ethanol:acetone (80:20); or 95% ethanol (with no acetone). 80 μ L of the solubilized CV was removed and added to a fresh polystyrene, 96-well dish, and OD₆₀₀ or OD₅₇₀ was determined using either a Series 700, Microplate Reader from Cambridge Technology, Inc.
10 or an MR 700 Microplate Reader from Dynatech Laboratories, Inc.

Growth curves were determined by subculturing (1:100) the relevant strain into the appropriate medium and growing the culture at room temperature without shaking. OD₆₀₀ readings were taken over time with a spectronic 20D+ from Spectronic Instruments, Inc.
15

Example II: Identification of mutations that affect biofilm formation in *Pseudomonas fluorescens*

Protein synthesis is required for biofilm formation.

There are marked differences in the profile of proteins synthesized
20 by biofilm-grown cells versus planktonic cells. We hypothesized that *P. fluorescens* synthesizes proteins required to form biofilms in response to appropriate signals. One of the predictions of such a model is that protein synthesis inhibitors should block biofilm formation in an environment that would otherwise promote this process. To test this prediction, cells were
25 incubated in the presence or absence of the protein synthesis inhibitor tetracycline (Tc, 150 μ g/ml) in microtiter wells for 30 minutes, after which the

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wells were developed with CV to assess biofilm formation using the rapid biofilm formation assay described above. As shown in Fig. 2, after 30 min, biofilm formation is strongly inhibited in the presence of 150 µg/ml Tc, compared to the untreated control (the extent of biofilm formation is expressed as the absorbance at 540 nm). This concentration of Tc does not reduce the numbers of viable planktonic cells (Tc-treated cultures, 1.0×10^8 CFU/ml; untreated control, 1.2×10^8 CFU/ml). This result indicates that new protein synthesis is required for *P. fluorescens* to form biofilms on an abiotic surface.

In contrast to the observation described above, continued protein synthesis is not required after the initial events of biofilm formation. Cells were first allowed to incubate in the microtiter wells for 30 minutes to form biofilms and then treated with Tc. After incubation for an additional 30 minutes in the presence of Tc, the microtiter dish wells were developed with CV to assess the extent of biofilm formation. There was no difference in biofilms (Fig. 2) or viable cell counts (not shown) between Tc-treated cells and untreated control cells.

These data suggest that the earliest events of biofilm development can be divided into two stages. The first stage, initial interaction with the abiotic surface, requires new protein synthesis. However, the subsequent stage (short-term maintenance of the attached cells) does not require synthesis of new proteins.

Extra-cytoplasmic proteins participate in biofilm formation.

Extra-cytoplasmic proteins, specifically those proteins on the surface of the bacterial cell, are thought to be important for bacterial attachment to abiotic substrates. To address the importance of such proteins in our biofilm system, we determined the effect of treatment with a protease, Pronase E

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(added upon inoculation of the cells into microtiter wells) on the formation of biofilms, using the rapid attachment assay. The number of attached cells was markedly decreased in the wells treated with Pronase E (~5-10-fold) compared to untreated control wells. In contrast, the counts of viable planktonic cells were similar under both conditions (average viable counts for untreated samples, 1.5×10^8 CFU/ml and Pronase E treated samples, 2.4×10^8 CFU/ml), indicating that treatment with protease did not decrease the number of viable cells. This result indicates that at least one extra-cytoplasmic protein is necessary for adherence to PVC.

10 **Environmental factors affect biofilm formation.**

Because the nutritional content of the medium can regulate biofilm development, we tested various nutrients for their effects on the ability of *P. fluorescens* to form biofilms on PVC. The following additions to minimal M63-based media promoted the formation of biofilms: 0.2% glucose, 0.2% glucose + 0.5% CAA, 0.2% glucose + 3 μ M FeSO₄, 0.5% CAA, 0.4% glutamate, 0.4% citrate, 0.4% malate, 0.4% mannitol, 0.4% xylose, and 0.4% glycerol. Although glucose alone does promote biofilm formation, the addition of iron or CAA stimulates biofilm formation by ~2- to 3-fold over glucose alone.

20 We assessed the effect of changes in osmolarity on the ability of *P. fluorescens* to form biofilms on PVC, using two osmolytes, NaCl and sucrose. The NaCl concentration was varied from 0 to 0.4 M in minimal medium supplemented with glucose and CAA. The growth of this strain was unaffected across this range of NaCl concentrations. However, at concentrations of NaCl at or above 0.2 M, biofilm formation was decreased by up to 4-fold, as assayed by CV staining. Cells grown in minimal medium as above, but supplemented

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with 0 to 20% sucrose, also grew to equal final optical densities. At sucrose concentrations of 15% or 20%, however, biofilm formation decreased by greater than 4-fold when compared to control cultures lacking sucrose. It is important to note that the osmolarity of the medium used in these experiments with 0.2 M NaCl is approximately equal to medium supplemented with 15% (~0.44 M) sucrose. Taken together, these data strongly suggest that growth in high osmolarity (and not simply ionic strength) inhibits biofilm formation by *P. fluorescens* on PVC. Variations in the starting pH (from 5.0 to 8.5) of the growth medium had no effect on biofilm formation after incubation for 10 hrs under standard assay conditions.

The results presented above show that environmental conditions and the nutritional status of the medium can influence biofilm formation. Furthermore, as demonstrated by the experiments in which osmolarity was varied, there are environmental conditions that promote cell growth, but do not promote significant biofilm formation.

Isolation of mutants defective in biofilm formation.

To isolate strains defective in biofilm formation on an abiotic surface, Tn5-based transposons that confer Tc^r or Gm^r (Simon, R., et al., 1989, *Gene* 80: 160-169) were used to mutagenize *P. fluorescens*. Of the ~14,000 transposon mutants screened, 37 mutants (0.3%) were unable to form a biofilm (Fig. 3; assay was developed after a 10 hour incubation) and had a growth rate indistinguishable from the wild-type strain in liquid medium. These mutants were designated surface attachment defective (*sad*). Twenty-eight of these mutants (23 motile and 5 non-motile) were analyzed further. Fig. 4A shows the quantitation of the biofilm formed by representative *sad* mutants on PVC. As described below, various growth conditions rescue the biofilm formation defect

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of some of the *sad* mutants. The subset of mutants presented in Fig. 4A-4D and in Table 2 was chosen to represent each of the phenotypic classes defined by the nutritional rescue experiments described below.

The biofilm formation screen described above was performed using microtiter dishes composed of PVC. However, it is clear that bacteria form biofilms on a wide range of abiotic surfaces. We tested the ability of wild type bacteria and selected mutants to form biofilms on relatively hydrophobic surfaces (PVC, polycarbonate, and polypropylene) and on a relatively hydrophilic surface (borosilicate glass). Wild type and mutant strains were allowed to form biofilms on these surfaces over a ten hour incubation period, then stained with CV and quantitated (Fig. 4A-4D). In general, mutants that were unable to form biofilms on PVC also were unable to form biofilms on the other surfaces tested, suggesting that a common genetic pathway is used to form biofilms on a range of abiotic surfaces. However, the strain carrying the *sad-10* allele is notable in that it has a biofilm formation defect on hydrophobic surfaces (PVC, polycarbonate, and polypropylene), but its biofilm formation phenotype on a hydrophilic surface (borosilicate glass) is indistinguishable from that of the wild type. In addition, the *sad-13* (*fliP*) mutant displayed a defect in biofilm formation on PVC, although this defect was less apparent on the other surfaces, especially polystyrene. In addition, the colony morphology of wild type bacteria vs. *sad* mutants was indistinguishable on LB medium.

Phenotypes of surface attachment defective mutants.

In order to further classify the *sad* mutants, they were assessed for the following phenotypes: growth in liquid medium, colony morphology, motility, fluorescent pigment production, biofilm formation under various

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environmental conditions, and determination of their molecular defects. The results of the phenotypic (and molecular) analyses of a representative subset of the *sad* mutants is summarized in Table 2.

The growth rate of all of the *sad* mutants in minimal medium supplemented with glucose and CAA (standard assay conditions) was identical to the wild type. None of the mutants were auxotrophs as judged by growth on minimal medium supplemented only with glucose. All mutants were also tested for their growth rate on minimal glucose/CAA + 3 μ M FeSO₄, minimal medium + citrate (0.4%), and minimal medium + glutamate (0.4%). Only those mutants whose growth rates were indistinguishable from the wild type growth rate under all growth conditions were analyzed further.

Motility is required for biofilm formation on biotic and abiotic surfaces. As expected, some of the mutants isolated were non-motile (Table 2, column 2). However, most of the strains were as motile as the wild type, yet had severe defects in the initiation of biofilm formation.

Many bacteria, including *P. fluorescens*, synthesize siderophores, phenazines, and other pigments. One of the *sad* mutants (*sad-21*) did not produce this strain's characteristic yellow-green pigment.

Table 2. Phenotypes and molecular analysis of selected *sad* mutants.

Allele	Biofilm Formation on PVC ^a	Motility	Pigment Production	Biofilm Formation: Rescue by Fe, Citrate & Glutamate ^b	Locus ^c
<i>sad</i> ⁺ (wild type)	+	+	+	+	na
<i>sad-10</i>	-	+	+	+	no match
<i>sad-11</i>	-	+	+	+	<i>clpP</i>
<i>sad-13</i>	-	-	+	+	<i>fliP</i>
<i>sad-14</i>	-	-	+	+	<i>flaE</i>
<i>sad-16</i>	-	-	+	+	nd
<i>sad-18</i>	-	+	+	-	no match
<i>sad-19</i>	-	+	+	nd	no match
<i>sad-20</i>	-	-	+	+	nd
<i>sad-21</i>	-	+	-	+	nd
<i>sad-22</i>	-	-	+	+	nd

^aThe medium used was M63 minimal medium supplemented with glucose and CAA.

^bRescue of the biofilm formation defect was assessed by growing the mutants on M63 minimal medium supplemented with citrate or glutamate at 0.4 %, or M63 minimal medium supplemented with glucose, CAA and 3 mM FeSO₄.

^cThe locus was determined by sequencing the DNA flanking the insertion element as described in the Experimental Procedures. If the flanking sequence was homologous to a known locus it is listed. "No match" indicates no significant similarity to any sequence on the database using the BLASTX program (Altschul, S.F., et al., 1990. *J. Mol. Biol.* 215: 403-410). Abbreviations: na, not applicable; nd, not determined.

^dThe biofilm formation defect of *sad-19* is rescued by the addition of citrate, but not by iron or glutamate.

Molecular characterization of *sad* mutants.

The DNA sequence flanking the insertion elements was determined for 24 of the 37 mutants (22 motile and 2 non-motile) in order to identify the gene(s) disrupted in each of the mutants. Typically, 200-400 bp of DNA sequence flanking the transposon insertions were obtained using the arbitrary PCR method. DNA flanking sequences were compared to sequences in Genbank using the BLASTX program (Altschul, S.F. et al., 1990, *J. Mol. Biol.* 215: 403-410). BLASTX translates the DNA sequence in all six reading frames and compares the translated sequences to sequences in Genbank. The results from analyses of selected mutants are presented in Table 2, column 6. Gene identifier sequences of selected *sad* mutants are shown in Fig. 9.

The mutants fall into three broad groups. The first group is comprised of motile strains having their mutation in a locus of known or proposed function. The strain carrying allele *sad-11* (*clpP*) comprises this class. The second group is comprised of non-motile strains, two of which were shown to have mutations in genes required for flagellar synthesis. The third group is comprised of motile strains, but unlike the first group, the DNA sequence flanking the transposon has no obvious similarity to any genes of known function in Genbank, as judged by the BLASTX program. This group of mutants included those having sequences that matched nothing in Genbank and those having sequences that matched genes of unknown function. Transposon insertions from two representative strains of this third group (*sad-18* and *sad-19*) were cloned and over 500 bp of DNA sequence flanking the transposon were determined. Again, no significant matches to genes of known function were found. In fact, only 3 of the 24 mutants analyzed had mutations in genes of known function. Two of these were non-motile mutants (*sad-13* and *sad-14*), in which matches to genes known to be required for synthesis of functional flagella were identified. Taken together,

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these results suggest that this genetic screen has allowed us to identify heretofore unknown genes.

Motility is conditionally required for biofilm formation.

Strains carrying alleles *sad-13* and *sad-14* (mutants originally isolated on minimal glucose/CAA medium) have transposon insertions in structural genes required for flagellar synthesis. It appears that we have identified the *P.*

fluorescens homolog of *fliP*. The identification was made based on the degree of similarity of the predicted polypeptide encoded by the DNA sequence flanking the insertion in the strain carrying allele *sad-13* to the *P. aeruginosa* PAK *fliP* gene (56% identity and 66% similarity over 77 aa). *FliP* is thought to participate in flagellar synthesis (Malakooti, J., et al., 1994, *J Bacteriol.* 176: 189-197) and is within an operon containing other flagellar biosynthetic genes, including *fliO*, which is required for non-pili mediated attachment to eukaryotic cells. Because *fliP* is probably part of a gene cluster required for flagellar synthesis, it is not

presently possible to conclude whether *fliP* and/or a downstream gene is responsible for the biofilm formation defect. The strain carrying allele *sad-14* contains a insertion in what appears to be the *P. fluorescens* homolog of the *flaE* gene of *Vibrio parahaemolyticus* (McCarter, L.L., 1995, *J. Bacteriol.* 177: 1595-1609) and the *flgK* gene of *Salmonella typhimurium* (Homma, M. et al., 1990, *J. Mol. Biol.* 213: 819-832). The predicted polypeptide (~70 aa) encoded by the sequence flanking the insertion in *sad-14* is ~40% identical and ~60% similar to the *flaE* and *flgK* genes. These genes are thought to encode a structural component of the flagellum. The isolation of multiple non-motile mutants that are also defective for biofilm formation on an abiotic surface shows that there is an overlap between factors required for biofilm formation on biotic and abiotic surfaces, and further validates our approach for isolating mutants defective in this

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process. As shown below, however, flagella-mediated motility only appears to be required under certain growth conditions.

The Clp protease participates in biofilm formation.

The DNA sequence flanking the insertion in the strain carrying *sad-11*, which is motile and is defective in forming biofilms on both hydrophilic and hydrophobic surfaces, encodes a polypeptide with high similarity (~80% identity and ~95% similarity over a 54 aa stretch) to the ClpP protein of *E. coli*, which is a subunit of the cytoplasmic Clp protease (Gottesman, S. and Maurizi, M.R., 1992, *Microbiol. Rev.* 56: 592-621). Based on this level of similarity, we propose that we have identified the ClpP protein homolog of *P. fluorescens*. The location of the transposon insertion in *clpP* is just downstream of the putative start of translation.

We performed complementation analysis to confirm that the mutation in *clpP* was causing the biofilm formation defect. The *clpP* gene of *E. coli* was amplified from chromosomal DNA of ZK126 (W3110 *clpP*⁺) by PCR and cloned into a vector (pSMC28) that is stably maintained in *Pseudomonas* spp. The resulting plasmid pSMC26 (*clpP*⁺), and the vector control (pSMC28), were introduced into wild-type *P. fluorescens* and the *sad-11* (*clpP*) mutant. These plasmid-carrying strains were then tested for biofilm formation. These data are summarized in Fig. 5. The first two columns of Fig. 5 show the biofilm formation phenotype of the wild-type and *clpP* strains (not carrying any plasmids). Complementation analysis (columns 3-6) revealed that the biofilm formation of the *clpP* mutant is completely rescued by providing a plasmid-borne copy of *clpP*⁺ derived from *E. coli* (column 5). The vector control has no effect on biofilm formation of the wild-type or *clpP* strain (columns 3 and 4).

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Providing *clpP* in multiple copies appears to have no adverse effects on biofilm formation by the wild-type strain.

We also directly assessed the ability of the *clpP* mutant carrying pSMC26 (*clpP*⁺) or the vector control (pSMC28) to attach to PVC, using phase contrast microscopy (Fig. 6; 600X magnification; assays performed in minimal glucose/CAA medium). The left panel of Fig. 6 shows multiple cells adhered to the PVC plastic when the *clpP* mutant is carrying pSMC26 (*clpP*⁺). This phenotype is similar to what is seen with the wild-type strain. When the *clpP* mutant carries just the vector control (Fig. 6, right panel) very few cells are found attached to the PVC plastic. These data are consistent with the indirect assessment of biofilm formation by CV-staining that are shown in Fig. 5, and demonstrate that the ClpP protein participates in biofilm formation.

Multiple signaling pathways participate in biofilm formation.

As discussed above, various nutritional conditions impact biofilm formation by *P. fluorescens*. Based on these observations, biofilm formation by the *sad* mutants (originally isolated on minimal medium supplemented with glucose and CAA) was assessed in a variety of media. The biofilm formation defect of approximately half of the *sad* mutants was rescued by growth on minimal medium supplemented with citrate or glutamate as the sole source of carbon and energy, or minimal glucose/CAA medium supplemented with 3 μ M FeSO₄.

Fig. 7 shows rescue of the biofilm formation defect of *sad* mutants. The extent of biofilm formation after 10 hrs of growth is expressed as the absorbance at 600 nm. Shown are the values for the wild type and selected *sad* mutants. The biofilm formation phenotype of the *sad* mutants was assessed with

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cells grown on minimal medium supplemented with: (i) glucose/CAA, glucose/CAA plus iron (3 mM), (ii) citrate (0.4%), or (iii) glutamate (0.4%).

The *sad* mutants could be divided into three classes based on their ability to be rescued by citrate, glutamate or iron-supplemented glucose/CAA medium (Fig. 7 and Table 2). One class (containing 12 mutants) represented by the strain carrying allele *sad-18*, showed a strong biofilm formation defect under all nutritional conditions tested. The second class, represented by the single strain carrying the *sad-19* allele, was rescued by growth on citrate, but not on glutamate or glucose/CAA + iron. The remainder of the *sad* mutants (10 mutants) were rescued for their biofilm formation defect when grown on minimal medium supplemented with citrate, glutamate, or glucose/CAA + iron.

Among the *sad* mutants rescued by growth on citrate, glutamate, or glucose/CAA + iron medium were the non-motile strains shown to carry mutations in the genes required for flagellar synthesis (see Table 2). It is important to note that growth on citrate, glutamate or iron-supplemented glucose medium, while restoring the cells' ability to form biofilms, does not restore motility as assayed on 0.3% motility agar plates. Furthermore, although 0.29% malate, mannitol, xylose, and glycerol promote biofilm formation 0.2%, these carbon sources did not rescue the biofilm formation defect of any of the *sad* mutants. Therefore, rescue of the biofilm formation defect was specific for particular growth conditions.

The growth of mutants in minimal glucose/CAA medium supplemented with CaCl_2 , MgSO_4 , and MnSO_4 (all provided at 3 μM) did not restore their ability to form biofilms, indicating that the ability to rescue the biofilm formation defect of the *sad* mutants is specific to iron. Taken together, these data show that multiple, convergent genetic pathways are involved in the

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early events of biofilm formation and these pathways can be induced by various, specific environmental signals.

Example III: Identification of mutations that affect biofilm formation in *Escherichia coli*

5 *E. coli* Forms Biofilms in a Nutrient-dependent Fashion.

We tested the ability of the well characterized, gram-negative bacterium, *E. coli*, to initiate biofilm formation on abiotic surfaces. To assay for such attachment, we used a modified version of a previously described protocol (Fletcher, M., 1977, *Can. J. Microbiol.*, 23, 1-6). Cells were first grown for either
10 24 or 48 hours at room temperature without shaking in microtiter dishes or glass tubes. In order to remove any unattached cells, the microtiter dishes (or glass tubes) were rinsed thoroughly with water and subsequently stained with 1.0% crystal violet (CV) for approximately 20 minutes. This staining procedure allowed us to visualize cells that had attached to an abiotic surface because
15 attached cells stain purple with CV whereas abiotic surfaces are not stained by CV. We found that a number of motile laboratory strains of *E. coli* were able to attach to multiple abiotic surfaces when grown in Luria Bertani broth (LB). Specifically, *E. coli* W3110 formed biofilms on all surfaces tested, including polyvinyl chloride (PVC), polypropylene, polycarbonate, polystyrene, and
20 borosilicate glass.

Importantly, the ability to form such biofilms was strongly influenced by the nutritional environment. Figure 10 shows the nutritional effects on biofilm formation. Wild-type cells were grown in PVC microtiter dishes in LB at room temperature without shaking for 24 hours, then subcultured (1:100) into
25 PVC microtiter dishes containing the indicated media. These cultures were

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grown for 48 hours at room temperature without shaking, then rinsed and stained with crystal violet. Biofilm formation could be visualized with CV after as little as two hours of growth in LB. Similarly, biofilm formation was supported by various minimal media containing casamino acids (CAA) (Fig.10). In contrast, minimal media without CAA (with either glucose or glycerol as a carbon and energy source) did not support biofilm formation that was visible after staining with CV (Fig.10).

Screen for *E. coli* Mutants Defective in Biofilm Formation.

To identify genes required for biofilm formation, we screened for mutants defective in forming biofilms in LB on PVC plastic. Strain W3110 was subjected to insertion mutagenesis (Kleckner, et al., *supra*) with a mini Tn10cam, and insertion mutants were selected on LB agar containing 30 µg/mL chloramphenicol.

Chloramphenicol resistant colonies were picked and grown at room temperature in 96-well PVC microtiter dishes containing glucose minimal medium with 30 µg/ml chloramphenicol. After 48 hours, the cells were subcultured into corresponding wells in a 96-well PVC microtiter dish containing LB with 30 µg/mL chloramphenicol. The cultures were grown at room temperature for another 48 hours and then rinsed thoroughly with water to remove any planktonic cells. The wells were stained with CV, rinsed, and potential biofilm-defective mutants were identified based on decreased staining compared to a wild-type control. Each potential biofilm-defective mutant was isolated from its original microtiter well, streaked for single colonies on LB agar, and re-tested for its ability to form a biofilm. Each of the insertion mutations that appeared to confer a defect in biofilm formation was transferred into a fresh W3110 background via P1 vir-transduction and re-tested. Of 10,000 such

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insertion mutations analyzed, 177 were found to confer a decrease in biofilm formation.

Initial Classification and Mutant Identification.

It is possible that a mutant strain isolated in the above screen could exhibit decreased biofilm formation because it harbors a mutation that either: (1) confers a non-specific growth defect that indirectly affects biofilm development, or (2) interferes in the formation of biofilms without interfering with the growth rate. To distinguish between these possibilities, mutant strains were grown in LB and their growth rates were compared to the wild type. Only strains exhibiting growth rates indistinguishable from the wild type are discussed below.

The mutant strains displayed a wide array of phenotypes with respect to the severity in their decreased ability to form biofilms. The macroscopic phenotypes ranged from wells that displayed subtle decreases in CV staining to wells that appeared completely clear after CV treatment. As an early step in characterization of the mutants, each was analyzed for its ability to swarm on LB motility agar (0.3% agar). Approximately one-half of the mutants (87/177) displayed a decreased ability to swarm, whereas the remaining mutants formed swarms that were indistinguishable from the wild type. The majority of the Swarm⁻ mutants were severely defective in their ability to form biofilms (i.e. clear wells after staining with CV). Such swarm assays do not always allow one to distinguish between defects in flagellar biosynthesis, motility, and/or chemotaxis. Thus, the following central question arose: Which of these three aspects of bacterial flagella/movement is critical to biofilm formation?

Among the remaining Swarm⁺ mutants, 23 displayed macroscopic phenotypes comparable to those observed with Swarm⁻ mutants (i.e. clear wells after staining with CV; see examples of mutants that display the clear well

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phenotype in Fig. 11), whereas the others displayed less severe phenotypes. In this initial study, we focused on the 23 Swarm⁺ mutants with the strongest phenotypes. The 23 mutants referred to above were found to be tightly linked to each other, as indicated by P1 vir-transduction using a nearby Tn10. The precise
5 locations of nine of the 23 insertion mutations within this linkage group were identified utilizing arbitrarily primed PCR followed by DNA sequence analysis. All nine insertions were located in genes encoding for the regulation or synthesis of type I pili. Specifically, independently isolated insertions were found in *fimB* (two alleles), *fimA*, *fimC*, *fimD* (three alleles), and *fimH*. Thus, a second question
10 arose: What is the role of type I pili in *E. coli* biofilm formation?

Motility, not Chemotaxis, is Critical for Biofilm Formation.

We reasoned that there are three mechanisms through which flagella might be required for biofilm formation. First, it is possible that flagella could be
15 directly required for attachment to abiotic surfaces, thus facilitating the initiation of biofilm formation (e.g. as with tethered cells). Alternatively, motility could be necessary to enable a bacterium to reach the surface (e.g. to move through surface repulsion present at the medium-surface interface). Also, motility might be required for the bacteria within a developing biofilm to move along the
20 surface, thereby facilitating growth and spread of the biofilm. Finally, it is possible that chemotaxis is required for the bacteria to swim towards nutrients associated with a surface.

Since flagellar synthesis, motility, and chemotaxis have been extensively studied in *E. coli* (Macnab, R.M., 1996, In Neidhardt, F.C., et al.
25 (ed.), *Escherichia coli and Salmonella typhimurium: Cellular and molecular biology* ASM Press, Washington, DC, Vol. 2, pp. 123-145; Stock, J.B. and Surette, M.G., 1996, In Neidhardt, F.C., et al. (ed.), *Escherichia coli and*

Salmonella typhimurium: Cellular and molecular biology ASM Press, Washington, DC, Vol. 2, pp. 1103-1129), well defined mutations that inhibit each of these three aspects of flagellar function are available. Accordingly, we obtained the following mutations: 1. *fliC::kan* (strains harboring this allele are
5 unable to synthesize flagellin) and *flhD::kan* (a master regulator of flagellar synthesis whose absence confers an inability to synthesize flagella), 2. *DmotA*, *DmotB* and *DmotAB* (lesions that do not inhibit flagellar biosynthesis, but render cells non-motile or paralyzed), 3. *DcheA-Z::kan* (strains harboring this lesion are motile, but non-chemotactic).

Each of these alleles was moved into W3110 via P1vir-transduction, and the resulting strains were analyzed for their ability to form biofilms. Construction of these strains provided us with the tools required to distinguish between the possible roles of flagella/motility/chemotaxis that were detailed above. Fig. 11 shows biofilm formation of wild-type and mutant strains. Cells
15 with the indicated genotypes were grown in PVC microtiter dishes in LB at room temperature without shaking for 24 hours, then subculture (1:50) into LB. These cultures were grown for 24 hours at room temperature without shaking, then rinsed and stained with crystal violet. This assay revealed that motile cells that are non-chemotactic (*DcheA-Z::kan*) appear to form biofilms indistinguishable
20 from their wild-type counterpart. In contrast, cells either lacking flagella (*fliC::kan*, *flhD::kan*) or possessing paralyzed flagella (*DmotA*, *DmotB*, or *DmotAB*) were severely defective in biofilm formation (Fig. 11).

Fig. 12 shows quantification of biofilm formation. Cells with the indicated genotypes were grown for 24 hours in PVC microtiter dishes
25 containing LB, then subcultured (1:50) into PVC microtiter dishes with LB. At the times indicated, the microtiter dishes were rinsed, stained with CV, and the amount of CV staining was quantified. When biofilm formation was quantified

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over time, it became very clear that, under these conditions, chemotaxis is completely dispensable for normal biofilm formation (Fig. 12). In contrast, cells either lacking complete flagella (*fliC::kan*) or possessing paralyzed flagella (*DmotA*, *DmotB*, or *DmotAB*) are severely hindered in the initial stages of biofilm formation (Fig.12).

More detailed analysis of the defects conferred by these alleles was obtained through microscopic analysis of cells attached (or the absence of such attached cells) to PVC following growth in LB Fig 13 (A-D). Cells with the indicated genotypes were grown in PVC microtiter dishes in LB at room temperature without shaking for 24 hours, then subculture (1:50) into microtiter dishes containing LB and a tab of PVC plastic. These cultures were grown for 24 hours at room temperature without shaking. The PVC tabs were then removed, rinsed, and the remaining cells were visualized via phase contrast microscopy (400X magnification). Panel A shows the wild-type strain W3110; Panel B shows the mutant strain W3110 *DcheA-Z::kan* (which is non-chemotactic); Panel C shows the mutant strain W3110 *FimH1::cam* (which lacks pili); and Panel D shows the mutant strain W3110 *flhD::kan* (which lacks flagella). As illustrated in Fig. 13B, motile cells that are non-chemotactic are able to form biofilms that are indistinguishable at the cellular level from the biofilms formed by wild-type cells. In contrast, non-flagellated or paralyzed cells attach poorly to PVC. Moreover, the few cells that do attach are often located in small, dense clusters of cells (Fig. 13D).

Type I Pili are Critical for Initial Attachment to Abiotic Surfaces.

As discussed above, the macroscopic analysis of biofilm formation of *fim* mutants was analogous to that observed with the motility defective mutants (i.e. clear wells after staining with CV) (Fig. 11). However, microscopic analysis

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of these mutants revealed distinct phenotypes. Specifically, *fim* mutants are even more dramatically defective in initial attachment than are the paralyzed and non-flagellated cells. As illustrated in Figure 13C, in most microscopic fields no attached cells were observed, and only infrequently were a few attached cells observed. This result indicates that type I pili are critical for initial interaction with abiotic surfaces such as PVC.

α -Methyl-D-Mannoside Inhibits Attachment to Abiotic Surfaces.

One of the insertions in the *fim* gene cluster is located in the final gene of the operon, *fimH*. Lesions in *fimH* have been reported to affect the length of the tip (fibrilla) of type I pili (Ottemann, K.M. and Miller, J.F., 1997, *Mol. Microbiol.*, 24, 1109-1117). In addition, *FimH* functions as a mannose-specific adhesion, allowing *E. coli* to interact specifically with mannose residues on eukaryotic cells, thus facilitating infections such as cystitis (Hanson, M.S. and Brinton, C.C., 1988, *Nature*, 332, 265-268.; Low, D et al, 1996, In Neidhardt, F.C., et al. (ed.), *Escherichia Coli and Salmonella Typhimurium: Cellular and Molecular Biology* ASM Press, Washington, D.C., Vol. 1, pp. 146-157.; Maurer, L. and Orndorff, P., 1987, *J. Bacteriol.*, 169, 640-645; Old, D.C., 1972, *J. of Gen. Microbiol.*, 71, 149-157). Consequently, it is possible that the altered structure of the fibrilla of type I pili in *fimH* mutants could interfere with normal attachment to abiotic surfaces. Alternatively, the mannose-specific adhesin may play a more direct role in attachment.

To further address the role of *FimH* in biofilm formation, we tested whether the presence of a non-metabolizable mannose analog, α -methyl-D-mannoside, affected the ability of the wild-type strain, W3110, to form biofilms on PVC. Fig. 14 shows the effects of α -methyl-D-mannoside on biofilm formation. Cells were grown for 24 hours without shaking at room

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temperature, and then subcultured (1:50) into PVC microtiter dishes with LB plus 0, 5, 15, 25, 50, or 100 mM α -methyl-D-mannoside. After nine hours at room temperature without shaking, the microtiter dishes were rinsed, stained with CV, and the amount of CV staining was quantified. As illustrated in Fig.14, α -methyl-D-mannoside inhibits biofilm formation in a concentration-dependent fashion. Importantly, α -methyl-D-mannoside does not inhibit growth rates. As a specificity control, we have shown that although mannose also has a similar effect as α -methyl-D-mannoside, glucose does not inhibit biofilm formation, and neither mannose nor glucose inhibits growth. It is also important to note that α -methyl-D-mannose inhibits biofilm development on all other abiotic surfaces tested, including polycarbonate, polystyrene, and borosilicate glass. It is reasonable to assume that these various surfaces do not resemble mannose.

Fig. 15 shows a model for initiation of *E. coli* biofilm formation. Motility may be required to overcome surface repulsion, thereby allowing initial surface contact. Type I pili are needed to establish stable attachment, perhaps through interactions between the type I adhesion, *FimH*, and the abiotic surface. Finally, motility may also enable attached, growing cells to migrate along the abiotic surface, thereby facilitating biofilm expansion.

Example IV: Identification of mutations that affect biofilm formation in

Pseudomonas aeruginosa

Isolation of mutants defective in biofilm formation.

We generated a collection of ~2400 random transposon mutants of *P. aeruginosa* PA14 using the transposon Tn5-B30(Tcr) (Simon, R. et al., 1989, *Gene*, 80, 160-169). This collection of *P. aeruginosa* mutants was screened in microtiter dishes made of polyvinylchloride (PVC) to test for their ability to form

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a biofilm on an abiotic surface. The cells were allowed to grow in the wells of the microtiter dishes in a minimal M63 medium supplemented with glucose and casamino acids (CAA) to assess their ability to form a biofilm, as described above in the previous Examples. The biofilm was detected by staining with crystal violet (CV), a purple dye which stains the bacterial cells, but does not stain the PVC plastic. After addition of CV and incubation at room temperature for ~10 min, excess CV and unattached cells were removed by vigorous and repeated washing of the microtiter plates with water. An example of the phenotype of the wild-type strain is shown in Fig. 16. The biofilm is observed as a ring of CV-stained cells which forms at the interface between air and medium. Under the growth conditions used in this experiment, the only electron acceptor available is oxygen. Therefore, the biofilm forms only where oxygen levels are highest, that is, at the interface between air and medium. Of the ~2400 mutants screened, 15 mutants (0.5%) unable to form such a biofilm were isolated. These mutants were designated surface attachment defective or *sad*. The biofilm formation phenotypes of representative *sad* mutants pilY1 (genbank (gb) accession no. L76605), *pilB* (gb-M32066), and *flgK* (gb-X51738) are also shown in Fig. 16.

Any strains exhibiting poor growth under these screening conditions might give the same phenotype as mutants unable to initiate formation of a biofilm. Therefore, all of the putative *sad* mutants were grown in liquid minimal M63 medium supplemented with glucose and CAA (the same medium used to screen for mutants). Of the 15 putative *sad* mutants tested, 13 grew as well as the wild-type strain, but were unable to form a biofilm. The other two putative *sad* mutants had severe growth defects relative to the wild type and were not analyzed further.

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We performed Southern blot analysis of the 13 *sad* mutants that did not form a biofilm to determine the number of transposon insertions in each strain. A PCR-generated DNA fragment from the IS50 of Tn5 was used to probe EcoRI-digested chromosomal DNA (there are no EcoRI sites in Tn5-B30). This analysis revealed a single hybridizing band for each strain, consistent with each *sad* mutant having only a single transposon insertion. The further analyses of two classes of mutants (totaling 8 of 13) isolated in this screen is presented below.

We tested the *P. aeruginosa sad* mutants for their ability to form a biofilm on abiotic surfaces other than PVC, including polystyrene, polycarbonate and polypropylene. The wild-type strain can form a biofilm on all of these surfaces. In contrast, all of the *sad* mutants originally isolated on PVC were also defective for biofilm formation on these other surfaces.

Non-motile mutants are defective in biofilm formation.

In addition to the phenotypic analyses described above, all *sad* mutants were assessed for their motility phenotype on 0.3% agar (minimal M63 medium supplemented with glucose and CAA). Fig. 17 shows an example of a motility assay. The flagella-mediated motility of the wild-type strain, representative pili-defective mutants (*pilB* and *pilC*), and non-motile mutants (*flgK*, *sad-39*, and *sad-42*) was assessed on minimal M63 glucose/CAA medium with 0.3% agar after ~24 hrs of growth at 25°C. Migration of the cells from the point of inoculation (observed as a turbid zone) indicates that the strain is proficient for flagellar-mediated motility.

Of the 13 mutants tested, three strains (*sad-36*, *sad-39*, and *sad-42*) were found to be non-motile (Fig. 17). In a typical experiment after 24 hrs of growth at room temperature, the wild type and two representative mutants

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defective in pili biogenesis (*pilB* and *pilC*) clearly migrated from the point of inoculation while the *sad-36*, *sad-39*, and *sad-42* strains did not.

One of these mutants, *sad-36*, was chosen for further analysis. The *sad-36::Tn5(Tcr)* insertion was mobilized into a wild-type genetic background by phage SN-T-mediated transduction as reported (Jensen, E.C., et al., 1998, *Appl. Environ. Microbiol.*, 64, 575-580). 18 of 18 *Tcr* transductants (indicating inheritance of the Tn5 element) were non-motile and unable to make a biofilm, demonstrating that the single insertion in this strain was responsible for the observed phenotypes. The DNA sequence flanking the Tn5 insertion in *sad-36* was determined using arbitrary PCR and compared to the Genbank database using BLASTX (Altschul, S.F., et al., 1990, *J. Mol. Biol.* 215: 403-410). BLASTX translates DNA sequence in all six reading frames and compares these predicted protein sequences to Genbank. The determined DNA sequence flanking the Tn5 element (~375 nt), when translated, revealed a partial ORF with ~40% identity and ~65% similarity to HAP1 (*flgK*), the flagellar-associated hook protein 1 of *Salmonella typhimurium* and *Escherichia coli*. Mutations in the *flgK* locus in these organisms results in the synthesis of an incomplete flagellum, which renders the strains non-motile (Homma, M., et al., 1990, *J. Mol. Biol.*, 213, 819-832). The localization of the Tn5 insert of the strain carrying the *sad-36* allele to a gene required for flagellar function is consistent with the non-motile phenotype of this strain.

Type IV pili are required for biofilm formation.

We analyzed the DNA sequence flanking the transposon inserts of the other *sad* mutants. Comparison of the translated DNA sequences flanking the Tn5 insertions in *sad* mutants to the Genbank database revealed that five strains carried mutations in genes required for the synthesis of type IV pili.

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Type IV pili are important for the adherence to and colonization of eukaryotic cell surfaces and are thought to play a role in pathogenesis. Four of the five mutants defective in type IV pili biogenesis identified in the screen had mutations in the *pilBCD* operon, which is thought to code for accessory factors required for pili assembly and function. The strains carrying alleles *sad-31*, *sad-33*, and *sad-34* have mutations in the *pilB* gene. The DNA sequence flanking the transposon insertions in *sad-33* and *sad-34* was identical, indicating that these two strains were probably siblings. The mutations carried in *sad-31* and *sad-33/sad-34* map to two different locations within *pilB*.

The strain carrying allele *sad-29* has a mutation in the *pilC* gene. Because the *pilBCD* locus may form an operon, it is possible that polarity onto *pilD* is actually causing the phenotype. However, it has been shown in *P. aeruginosa* PAO1 that mutations in any of these loci result in the loss of the synthesis of pili as indicated by resistance to the pilus-specific bacteriophage PO4 and visual inspection by electron microscopy. (Nunn, D., et al., 1990, *J. Bacteriol.*, 172, 2911-2919).

The fifth mutant, *sad-25*, maps to yet a third locus, a homolog of the *pilY1* gene of *P. aeruginosa* PAO1. In *P. aeruginosa*, the *pilY1* gene is in a cluster of genes (including *pilV*, *pilW*, *pilX*, *pilY2*, and *pilE*) that are required for type IV pili biogenesis. Consistent with the mapping of these mutations to genes required for type IV pili biogenesis was their resistance to lysis by phage F116 (Pemberton, J.M., 1973, *Virology*, 55, 558-560), which utilizes type IV pili as its receptor.

It has been shown that type IV pili are required for a form of surface-associated movement known as twitching motility. Twitching motility is thought to be a consequence of the extension and retraction of type IV pili, which

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propels the bacteria across a surface by an undescribed mechanism (Bradley, D.E., 1980,

Can. J. Microbiol., 26, 146-154; Darzins, A., 1994, *Mol. Microbiol.*, 11, 137-153.; Whitchurch, C.B., 1990. *Gene*, 101, 33-44). We assessed the

5 twitching motility phenotype of the mutants carrying alleles *sad-25* (*pilY1*), *sad-29* (*pilC*), *sad-31* (*pilB*), and *sad-33* (*pilB*). The wild-type, a representative flagellar mutant (*flgK*), and four type IV pili mutants are shown in Fig. 18.

To assess twitching motility, cells were stabbed into an LB agar plate (1.5% agar) with a toothpick, incubated overnight at 37°C, then for 1-2 days at
10 room temperature (~25°C). Twitch⁺ strains form a colony on the agar surface and form a hazy zone of cell growth within the agar substrate. Twitch⁻ strains still form a colony on the agar, but lack the zone of growth within the agar. Also, the colonies of Twitch⁺ strains are flat, spreading, and irregularly shaped, while the colonies formed by strains defective in the synthesis of type IV pili are
15 rounded and somewhat dome-shaped.

In addition to forming a colony on the surface of the agar plate (1.5% agar), Twitch⁺ strains of *P. aeruginosa* PA14 form a haze of growth that surrounds the point of inoculation. This assay differs from the test for flagella-mediated motility, which is performed by inoculating cells onto 0.3%
20 agar plates (see Fig. 17). Furthermore, strains capable of twitching motility have a spreading colony morphology while strains defective in twitching motility produce rounded colonies. This difference in colony shape can also be observed in Fig. 18.

Twitching motility can also be assessed by phase-contrast microscopy.
25 At the microscopic level, the edge of the colonies of strains proficient in twitching motility are highly irregular. This is thought to be a consequence of the surface movement associated with type IV pili. Mutants lacking functional

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type IV pili have smooth-edged colonies. To further confirm that our strains did not have functional type IV pili, we observed the edges of wild-type and pili-deficient mutants by phase contrast microscopy. As shown in Fig. 19 (micrographs are at 400X magnification), the wild-type strain has the expected irregular colony edge and the representative pili-deficient strain (*sad-31/pilB*) has the expected smooth colony edge phenotype. All the pili-defective mutants behaved in a fashion identical to *sad-31*. Transmission electron microscopic analysis of the pili mutants confirmed the lack of these structures on the surface of the mutant cells.

Mutants defective in flagellar-mediated motility and type IV pili biogenesis define two steps in a developmental pathway. We utilized the *sad* mutants isolated in this study as tools to initiate the dissection of the early steps in biofilm formation. In order to follow the initiation of biofilm formation by the wild-type and *sad* mutants, we directly visualized the formation of the biofilm on PVC using phase contrast microscopy. A small tab of PVC plastic (~3mm x ~6mm) was incubated in the well of a microtiter dish that had been inoculated with 10^6 CFU/mL of the appropriate strain in minimal M63 medium supplemented with glucose and CAA. After incubation for various times at 37°C, the plastic tab was removed from the microtiter dish with ethanol-sterilized forceps, rinsed with 1 mL of sterile minimal M63 medium, placed on a slide, and examined by phase-contrast microscopy (400X magnification).

Fig. 20 shows a time course of the development of a biofilm on PVC by the wild-type strain over 7.5 hrs at 37°C as observed by phase-contrast microscopy. As early as 30 minutes after inoculation, the wild type formed a dispersed monolayer of bacterial cells attached to the surface of the PVC plastic. A progressively more dense monolayer of cells formed on the surface over the next 3-4 hours. By 5 hours, and continuing until at least 7.5 hours, this

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monolayer almost completely covered the PVC surface and became punctuated by micro-colonies (indicated by arrows) which were distributed across the surface of the PVC plastic and were comprised of multiple layers of cells. Typically, the wild-type micro-colonies were ~3-5 layers of cells thick.

5 We directly visualized the ability of the type IV pili-deficient and non-motile strains to form a biofilm on PVC using phase-contrast microscopy and compared their phenotypes to the wild-type strain. Fig. 21 shows phase-contrast photomicrographs of the wild-type strain, a representative pili-defective mutant (*flgK*), and a representative non-motile mutant (*pilB*) after incubation for 10 3 hours at 37°C in the presence of PVC plastic. Micrographs were taken at 400X magnification; approximately 50 fields were searched for each strain tested, and representative fields are shown. For the representative non-motile strain (carrying a mutation in *flgK*), few to no cells were observed attached the PVC plastic even after 8 hrs of incubation in the presence of the PVC surface (Fig. 15 21). All other non-motile strains analyzed had a phenotype identical to the *flgK* mutant.

We also directly visualized the biofilm formation phenotype of a representative mutant defective in pili biogenesis (*pilB*). At the early time points (< 3 hrs), there was little difference in the biofilm formation phenotype of the 20 wild type and the type IV pili mutants; both the wild-type and the pili-defective strain form a dispersed monolayer of cells on the surface of the PVC plastic. By 8 hours, in contrast to the aggregates of cells formed by the wild-type strain, the pili-defective mutants did not develop these characteristic micro-colonies (Fig. 21). Furthermore, the wild-type strain almost completely covered the PVC 25 surface with a dense, tightly-packed layer of cells (Fig. 21). The phenotype of the type IV pili mutants at this 8 hour time point was unchanged from that

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observed at 3 hrs, that is, a dispersed monolayer of cells. The other mutants defective in pili biogenesis (*pilC* and *pilYI*) had similar phenotypes.

A role for twitching motility in biofilm formation.

5 To better define the events that lead to micro-colony formation by the wild type and to determine if surface-based twitching motility plays a role in biofilm formation, we employed phase-contrast time-lapse microscopy to follow a developing biofilm. Utilizing time-lapse microscopy, we watched individual micro-colonies formed by the wild-type strain over a period of 56 minutes (with
10 images acquired at 15 second intervals). Shown in Figs. 22A-22I is a montage of 9 phase-contrast micrographs taken during biofilm formation by the wild-type strain every 7 minutes between 360 and 416 minutes post-inoculation. Arrows indicate micro-colonies that form and/or disperse over the course of the experiment. The black circles indicate the identical spot on the field in panels H and I. Several micro-colonies were followed through the course of this
15 experiment to illustrate the movement of cells across the PVC plastic surface.

In Figs. 22A-22I, the white arrow indicates the position of a micro-colony which is first clearly visible in Fig. 22B, becomes larger (Fig. 22C), but has dispersed by Fig. 22D. This micro-colony does not reform during
20 the course of this experiment (Figs. 22D through 22I). A series of time-lapse micrographs taken at 15 second intervals between 374 minutes (Fig. 22C) and 381 minutes (Fig. 22D) show that this micro-colony disperses because the cells comprising the colony move apart, while still remaining associated with the plastic surface.

25 The black arrow points to a large micro-colony evident in Fig. 22A. This large micro-colony becomes progressively smaller (Figs. 22B through 22F) and eventually splits into two small, adjacent micro-colonies (Fig. 22G). In Fig.

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22H, these two adjacent micro-colonies form a larger single colony which has grown slightly in size when visualized 7 minutes later (Fig. 22I).

The formation of micro-colonies in this system is due in large part to the aggregation of cells found dispersed in the monolayer of cells on the surface and not solely to the growth of the bacterial cells. This point is further illustrated by data presented in Figs. 22H and 22I. The dark circle in Fig. 22I indicates a dense, well-formed micro-colony. However, this colony is not evident 7 minutes previously in Fig. 22H. The elapsed 7 minutes between the micrograph shown in Fig. 22H and the micrograph shown in Fig. 22I represents less than the time needed for a single population doubling under these growth conditions. Furthermore, analysis of the time-lapse film shows that this micro-colony forms by recruiting adjacent cells from the monolayer. The data described above and shown in Figs. 22A-22I demonstrate the dynamic nature of micro-colony formation and dispersal during the course of biofilm development.

As discussed above, type IV pili are required for surface based twitching motility and mutants defective in type IV pili biogenesis do not make the micro-colonies characteristic of the wild-type strain. It is important to note that none of the behaviors described above for the wild-type were observed in the representative type IV pili mutant, *pilB*. As shown above in Fig. 21, this strain does not form micro-colonies when observed either after 8 hrs of growth or when monitored by time-lapse microscopy.

Fig. 23 shows a model for the role of flagella and type IV pili in *P. aeruginosa* biofilm formation. Flagella or flagella-mediated motility appear to be important for the formation of a bacterial monolayer of the abiotic surface. Type IV pili appear to play a role in downstream events such as micro-colony formation.

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Other Embodiments

5 All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each independent publication or patent application was specifically and individually indicated to be incorporated by reference.

10 While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure come within known or customary practice within the art to which the invention pertains and may be applied to the essential features hereinbefore set forth, and follows in the scope of the appended claims.

What is claimed is:

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1. A purified nucleic acid comprising a region that hybridizes under high stringency conditions to a probe comprising at least 75 consecutive nucleotides that are complementary to a portion of an *n-sad* gene, wherein said region comprises at least 75 consecutive nucleotides.

5 2. The nucleic acid of claim 1, wherein said *n-sad* gene is a *Pseudomonas fluorescens sad* gene, and wherein said *Pseudomonas fluorescens sad* gene comprises a sequence chosen from SEQ ID NOs: 1-24.

3. The nucleic acid of claim 1, wherein said nucleic acid is contained within an expression vector.

10 4. The nucleic acid of claim 1, wherein said nucleic acid encodes a polypeptide that has a biological activity necessary for biofilm formation under at least one condition known to allow biofilm formation by a bacterium that expresses said polypeptide.

15 5. A probe comprising at least 18 nucleotides that are complementary to an *n-sad* gene, wherein said *n-sad* gene is a *Pseudomonas fluorescens n-sad* gene, wherein said *Pseudomonas fluorescens n-sad* gene comprises a sequence chosen from SEQ ID NOs: 1-24.

20 6. The probe of claim 5, wherein said probe comprises at least 25, 40, 60, 80, 120, 150, 175, or 200 nucleotides that are complementary to said *n-sad* gene.

7. A substantially pure *n-sad* polypeptide.

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8. The polypeptide of claim 7, wherein said polypeptide has a biological activity necessary for biofilm formation under at least one condition known to allow biofilm formation by a bacterium that expresses said polypeptide.

5 9. A substantially pure antibody that specifically binds an *n-sad* polypeptide.

10 10. The polypeptide of claim 7 or 9, wherein said polypeptide comprises a polypeptide encoded by a *Pseudomonas fluorescens n-sad* gene, wherein said *Pseudomonas fluorescens n-sad* gene comprises a sequence chosen from SEQ ID NOs: 1-24.

11. A method of screening for a compound that modulates biofilm formation, said method comprising:

a) contacting a sample with a test compound, wherein said sample contains a *sad* gene, a *sad*/reporter gene, or a *sad* polypeptide, and

15 b) measuring the level of *sad* biological activity in said sample, wherein an increase in *sad* biological activity in said sample, relative to *sad* biological activity in a sample not contacted with said test compound, indicates a compound that increases biofilm formation, and a decrease in *sad* biological activity in said sample, relative to *sad* biological activity in a sample not
20 contacted with said test compound, indicates a compound that decreases biofilm formation.

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12. The method of claim 11, wherein said sample comprises bacterial cell extract.

13. The method of claim 11, wherein said *sad* gene, said *sad*/reporter gene, or said *sad* polypeptide is within a bacterial cell.

5 14. The method of claim 11, wherein said *sad* gene, said *sad*/reporter gene, and said *sad* polypeptide are from *Pseudomonas fluorescens*, wherein said *sad* gene and said *sad*/reporter gene comprise a sequence chosen from SEQ ID NOs: 1-24, and wherein said *sad* polypeptide is encoded by a gene comprising a sequence chosen from SEQ ID NOs: 1-24.

10 15. A method of screening for a compound that modulates biofilm formation, said method comprising:

 a) contacting a sample with a test compound, wherein said sample contains a *clpP* gene, a *clpP*/reporter gene, or a ClpP polypeptide, and

 b) measuring the level of ClpP activity in said sample, wherein an
15 increase in ClpP activity in said sample, relative to ClpP activity in a sample not contacted with said test compound, indicates a compound that increases biofilm formation, and a decrease in ClpP activity in said sample, relative to ClpP activity in a sample not contacted with said test compound, indicates a compound that decreases biofilm formation.

20 16. The method of claim 15, wherein said *clpP* gene, said *clpP*/reporter gene, or said ClpP polypeptide is a non-*E. coli clpP* gene, a non-*E. coli clpP*/reporter gene, or a non-*E. coli* ClpP polypeptide.

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17. The method of claim 15, wherein said sample comprises bacterial cell extract.

18. The method of claim 15, wherein said *clpP* gene, said *clpP*/reporter gene, or said ClpP polypeptide is within a bacterial cell.

5 19. The method of claim 18, wherein said bacterial cell is cultured under standard biofilm assay conditions after said contacting.

20. The method of claim 15, wherein said *clpP* gene, said *clpP*/reporter gene, or said ClpP polypeptide is from *Pseudomonas fluorescens*.

10 21. The method of claim 15, wherein ClpP activity is measured by measuring biofilm formation.

22. A method for preventing a bacterial cell from participating in formation of a biofilm, said method comprising a step selected from the group consisting of: inhibiting the synthesis or function of a *sad* polypeptide; inhibiting protein synthesis in said bacterial cell; contacting said bacterial cell with a
15 protease, wherein said contacting is sufficient to prevent said bacterial cell from participating in formation of a biofilm; limiting the concentration of $\text{Fe}^{2+}/\text{Fe}^{3+}$ in the environment of said bacterial cell, wherein the $\text{Fe}^{2+}/\text{Fe}^{3+}$ concentration in said environment is limited to 0.3 μM or less; providing a high osmolarity environment to said bacterial cell, wherein said osmolarity of said environment is
20 equivalent to or greater than the osmolarity of a solution containing 0.2 M NaCl or 15% sucrose; adding mannose to the environment of said bacterial cell, such that the mannose concentration in said environment after the addition of said

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mannose is at least 15 mM; and adding α -methyl-D-mannoside to the environment of said bacterial cell, such that the α -methyl-D-mannoside concentration in said environment after the addition of said α -methyl-D-mannoside is at least 15 mM.

5

23. The method of claim 22, wherein *sad* polypeptide is encoded by a *Pseudomonas fluorescens sad* gene.

10

24. The method of claim 22, wherein said mannose concentration or said α -methyl-D-mannoside concentration is at least 15 mM, 25 mM, 50 mM, or 100 mM.

25. The method of claim 22, wherein said surface is an abiotic surface.

15

26. The method of claim 13, 18, or 22, wherein said bacterial cell is selected from the group including: *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus* species, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus hominis*, *Staphylococcus haemolyticus*, *Staphylococcus warneri*, *Staphylococcus cohnii*, *Staphylococcus saprophyticus*, *Staphylococcus capitis*, and *Staphylococcus lugdunensis*.

20

27. A method for inhibiting participation of a bacterium in formation of a biofilm on a surface, said method comprising inhibiting the synthesis or function of a flagellum on said bacterium.

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28. The method of claim 27, wherein said surface is abiotic.

29. The method of claim 27, wherein said synthesis or function of said flagellum is inhibited by inhibiting the synthesis or function of: FliC (SEQ ID NO: 34); FlhD (SEQ ID NO: 35); MotA (SEQ ID NO: 36); MotB (SEQ ID NO: 37); FliP (SEQ ID NO: 38); FlaE (AB 001340; SEQ ID NO: 39); or FlgK (SEQ ID NO: 40); or homologues thereof.

30. A method for inhibiting participation of a bacterium in formation of a biofilm on an abiotic surface, said method comprising inhibiting the synthesis or function of a pilus on said bacterium.

31. The method of claim 30, wherein said function of said pilus is inhibited by contacting said pilus with mannose or α -methyl-D-mannoside.

32. The method of claim 30, wherein said synthesis or said function of said pilus is inhibited by inhibiting the synthesis or function of: PilB (SEQ ID NO: 41); PilC (SEQ ID NO: 42); PilD (SEQ ID NO: 43); PilV (SEQ ID NO: 44); PilW (SEQ ID NO: 45); PilX (SEQ ID NO: 46); PilY1 (SEQ ID NO: 47); PilY2 (SEQ ID NO: 48); or PilE (SEQ ID NO: 49); or homologues thereof.

33. The method of claim 30, wherein said bacterium is chosen from the group including: *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus* species, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus hominis*, *Staphylococcus haemolyticus*, *Staphylococcus warneri*, *Staphylococcus cohnii*,

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Staphylococcus saprophyticus, *Staphylococcus capitis*, and *Staphylococcus lugdunensis*.

34. A method of screening for a compound that inhibits bacterial pathogenicity, said method comprising:

5 a) exposing a bacterial culture to a test compound, such that at least one bacterial cell in said bacterial culture are contacted by said test compound, and

10 b) testing said bacterial culture for biofilm formation on an abiotic surface, wherein a decrease in biofilm formation, relative to biofilm formation by a bacterial culture that has not been exposed to said test compound, indicates a compound that inhibits biofilm formation, and an increase in biofilm formation, relative to biofilm formation by a bacterial culture that has not been exposed to said test compound, indicates a compound that stimulates biofilm formation.

15 35. The method of claim 34, wherein said bacterial culture is a liquid bacterial culture.

36. The method of claim 34, wherein at least 5%, 10%, 25%, 50%, 75%, or 100% of the bacterial cells contacted by the bacterial growth medium in said culture are contacted by said test compound.

20 37. The method of claim 34, wherein said bacterium is chosen from the group including: *Pseudomonas fluorescens*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Vibrio parahaemolyticus*, *Salmonella typhimurium*, *Streptococcus mutans*, *Enterococcus species*, *Serratia marcescens*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Staphylococcus hominis*,
25 *Staphylococcus haemolyticus*, *Staphylococcus warneri*, *Staphylococcus cohnii*,

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Staphylococcus saprophyticus, *Staphylococcus capitis*, and *Staphylococcus lugdunensis*.

38. A method of stimulating formation of a biofilm by a population of bacteria, said method comprising at least one of: adding iron to the growth
5 environment of said bacteria, such that the final concentration of said iron in said growth environment is at least 3 μ M; adding glutamate to the growth environment of said bacteria, such that the final concentration of said glutamate in said growth environment is at least 0.4%; adding citrate to the growth
10 environment of said bacteria, such that the final concentration of said citrate in said growth environment is at least 0.4%; and stimulating expression of a *sad* gene or activity of a *sad* polypeptide.

39. The method of claim 38, wherein said population comprises *Pseudomonas fluorescens*.



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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : A61K 39/395, 39/00, 39/38, 39/02, 39/108, C12Q 1/00, C12N 9/00, C07H 21/02, 21/04		A1	(11) International Publication Number: WO 99/55368 (43) International Publication Date: 4 November 1999 (04.11.99)
(21) International Application Number: PCT/US99/09034 (22) International Filing Date: 27 April 1999 (27.04.99) (30) Priority Data: 60/083,259 27 April 1998 (27.04.98) US 60/102,870 2 October 1998 (02.10.98) US (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications US 60/083,259 (CIP) Filed on 27 April 1998 (27.04.98) US 60/102,870 (CIP) Filed on 2 October 1998 (02.10.98) (71) Applicant (for all designated States except US): PRESIDENT AND FELLOWS OF HARVARD COLLEGE [US/US]; 17 Quincy Street, Cambridge, MA 02138 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): O'TOOLE, George, A. [US/US]; 14 Palace Road #2, Boston, MA 02115 (US). KOLTER, Roberto [US/US]; 741 Heath Street #3, Chestnut Hill, MA 02167 (US).		(74) Agent: BIEKER-BRADY, Kristina; Clark & Elbing LLP, 176 Federal Street, Boston, MA 02110-2214 (US). (81) Designated States: CA, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(54) Title: REGULATION OF BIOFILM FORMATION			
(57) Abstract The invention features novel genes involved in biofilm formation, methods for regulating biofilm formation, and methods of screening for compounds that modulate biofilm formation.			



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(54) Title: REGULATION OF BIOFILM FORMATION (57) Abstract The invention features novel genes involved in biofilm formation, methods for regulating biofilm formation, and methods of screening for compounds that modulate biofilm formation.		

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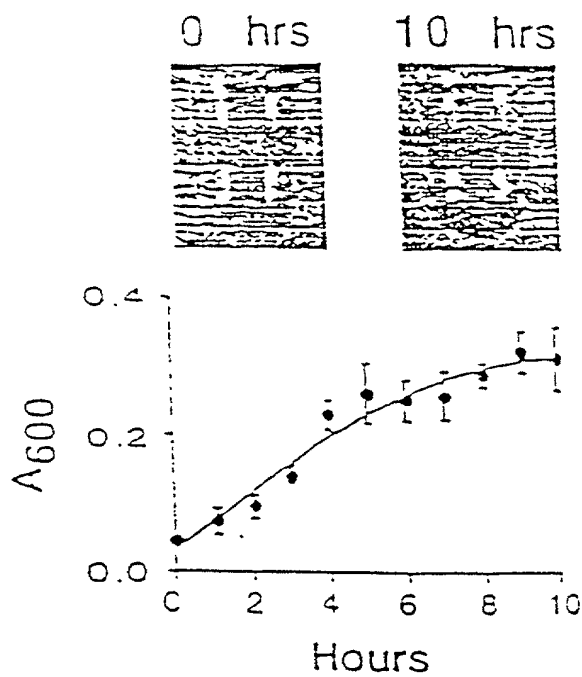


FIG. 1

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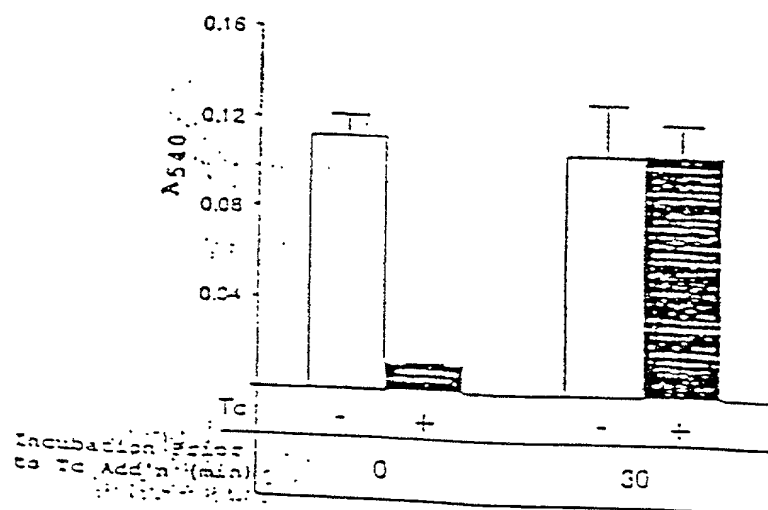


FIG. 2

wild-type : sad-1 1

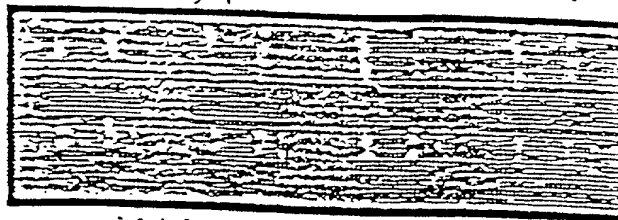


FIG. 3

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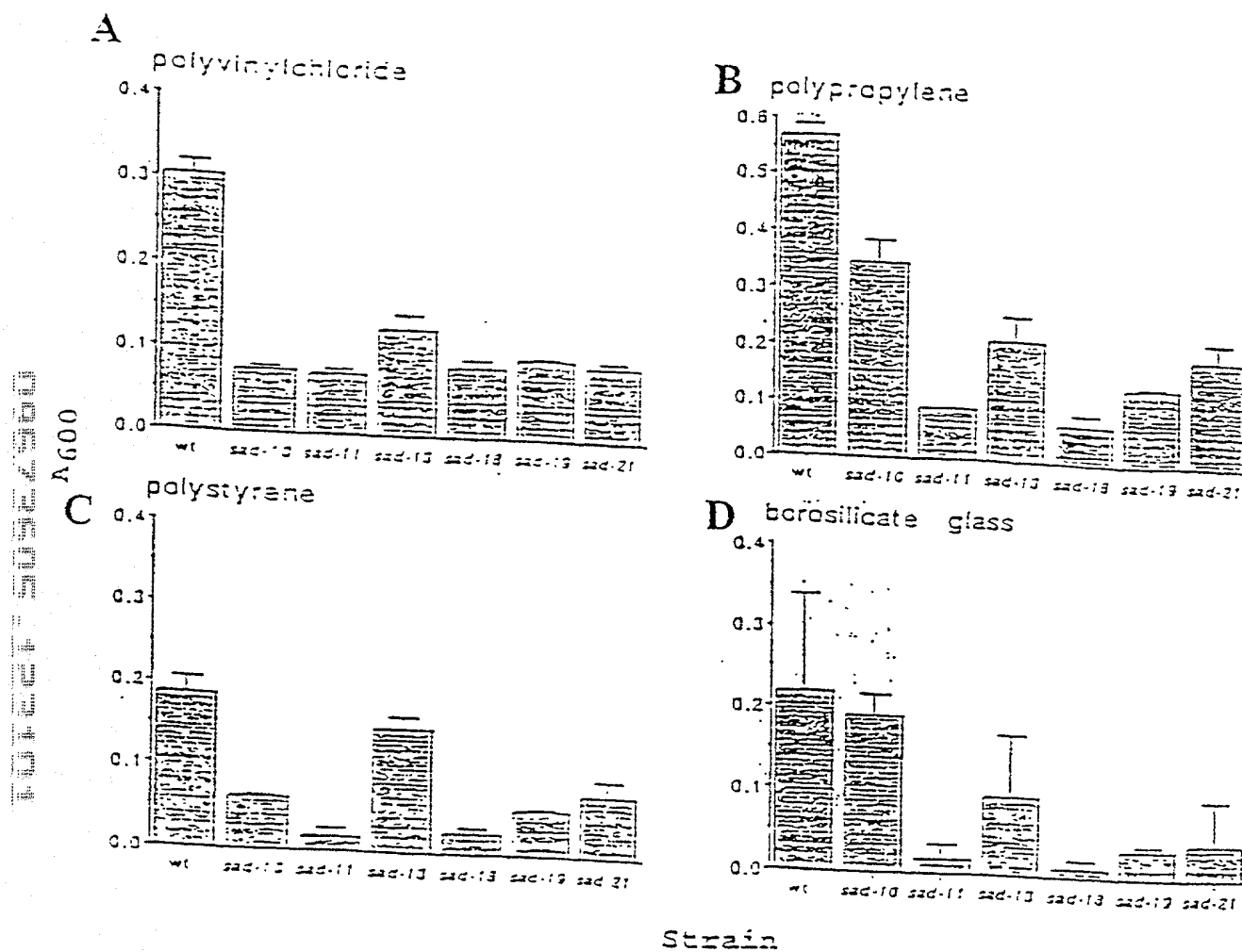


Fig. 4

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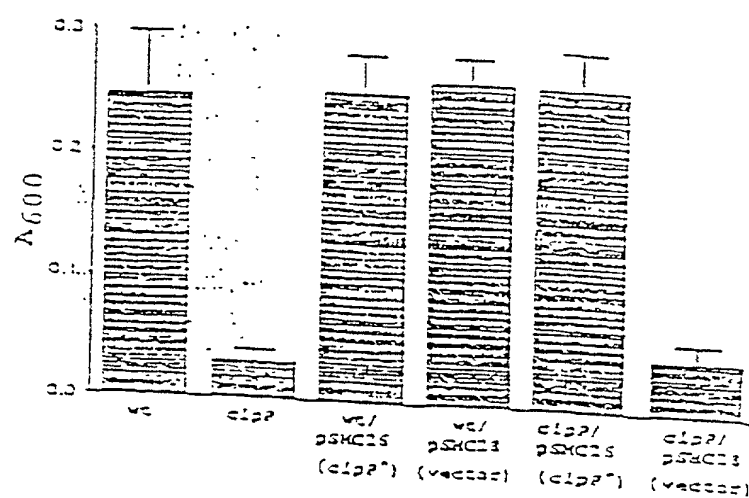


Fig. 5

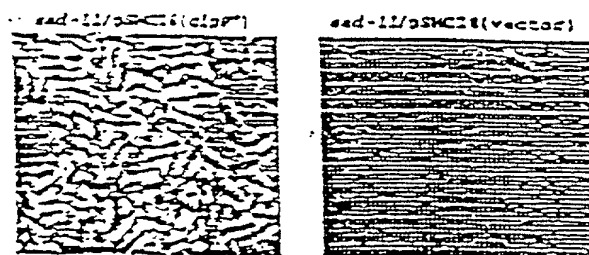


Fig. 6

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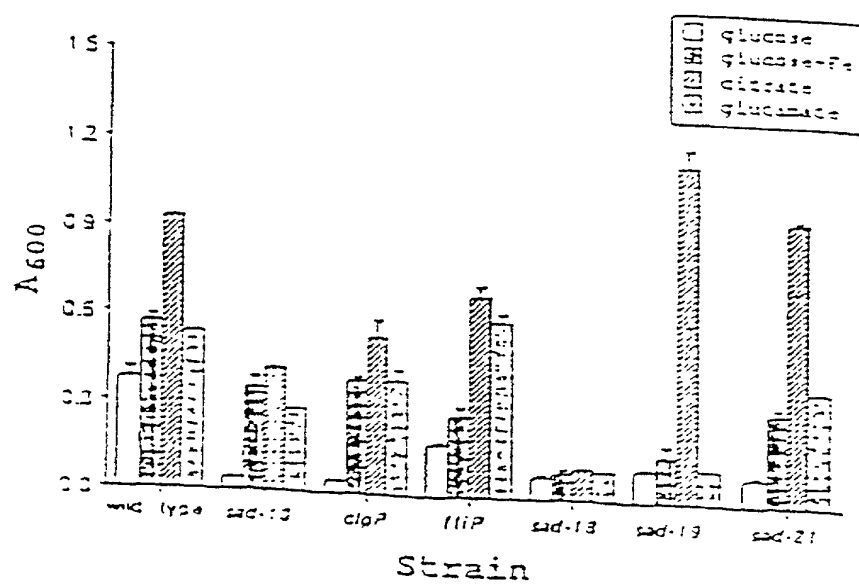


Fig. 7

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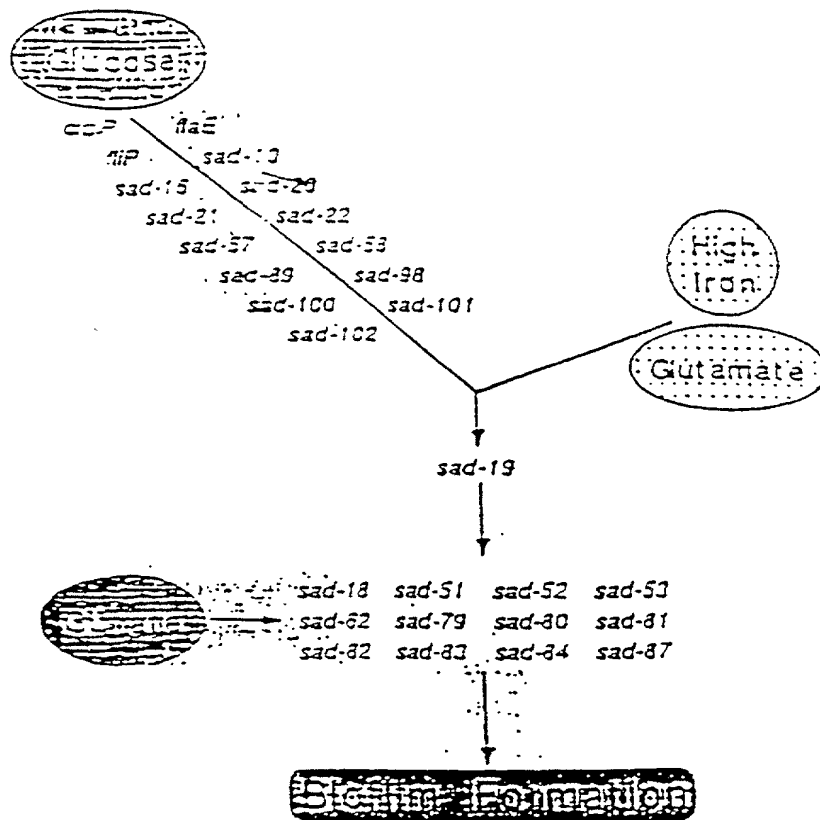


Fig. 8

seq-13 SEQ ID NO: 4

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10/34

s3d-13 SEQ ID NO: 5

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13/10
4

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WO 99/55368

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sac-21 SEQ ID NO: 7

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>sad-10 SEQ ID NO: 1

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15/34

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>sad-58 SEQ ID NO: 13

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WO 99/55368

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>sad-80 SEQ ID NO: 16

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WO 99/55368

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>sad-100

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>sad-101

SEQ ID NO: 23

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>sad-102

SEQ ID NO: 24

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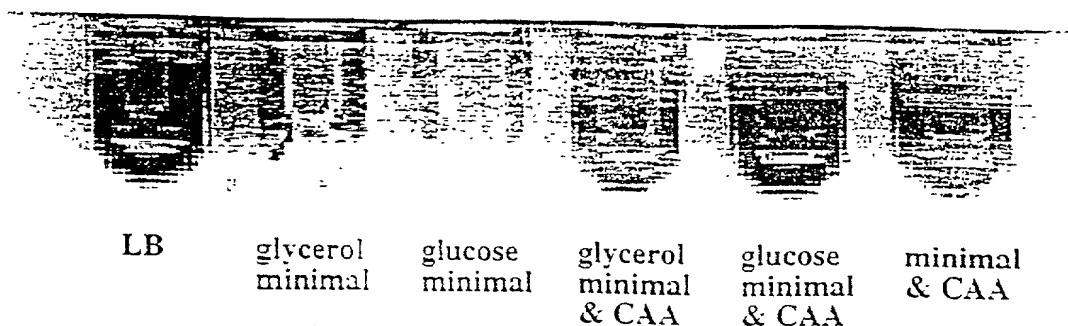


Fig. 10

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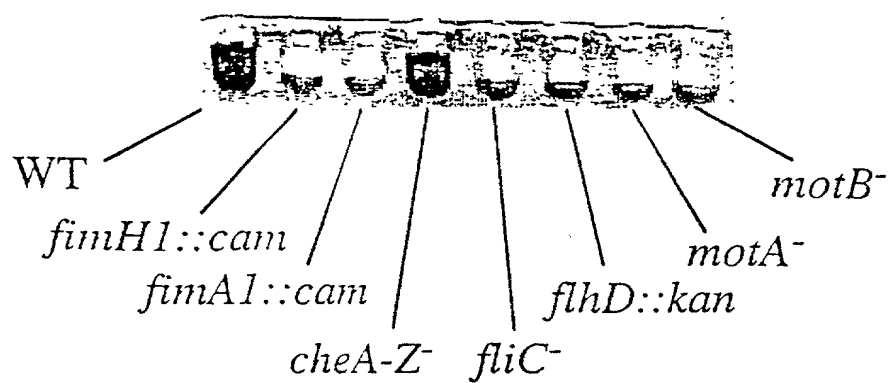
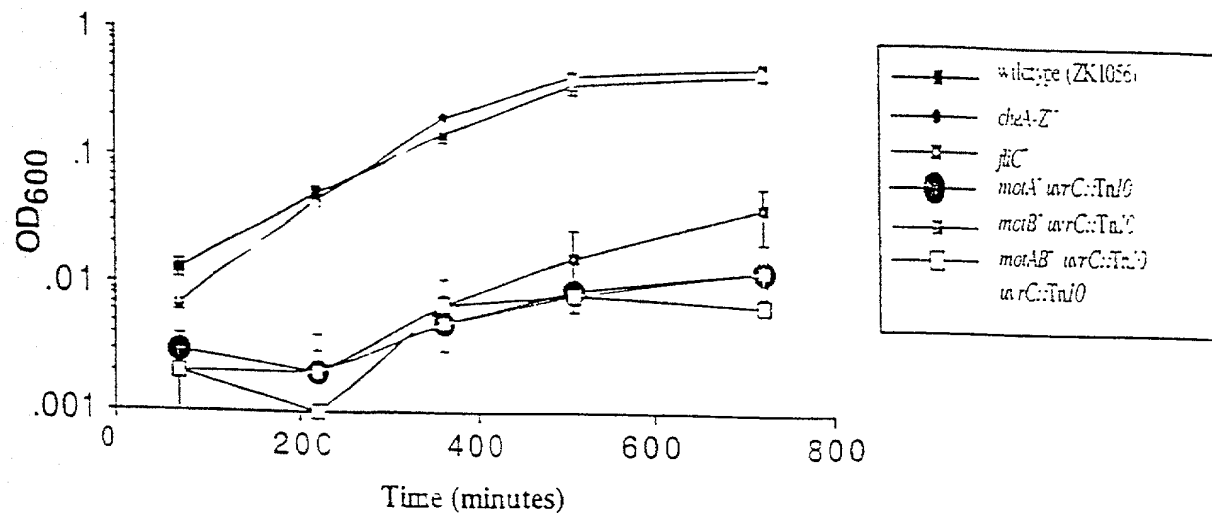


Fig. 11

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WT

*cheA-Z⁻ fliC⁻ motA⁻ motB⁻ motAB⁻*

Fig. 12

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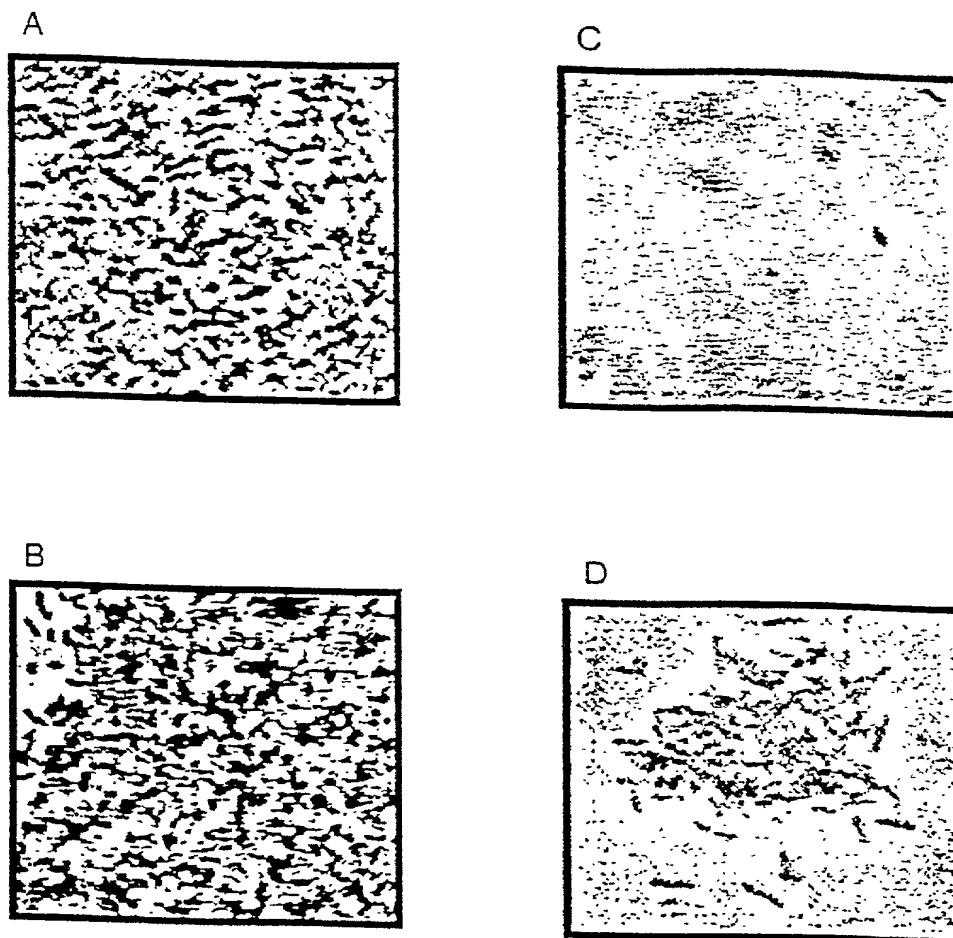


Fig. 13

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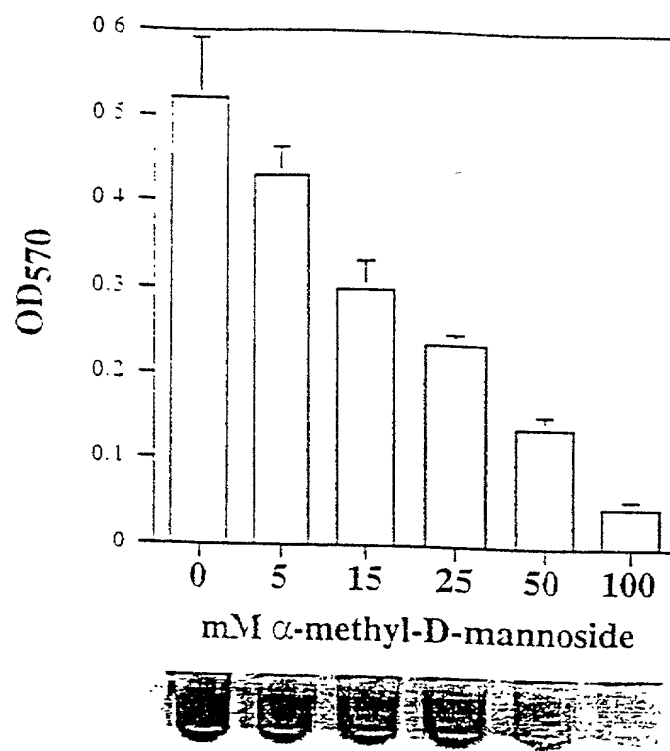


Fig. 14

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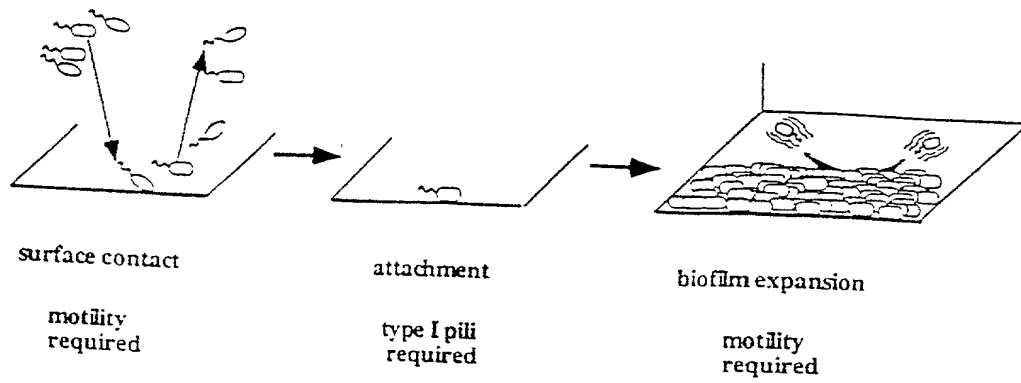


Fig. 15

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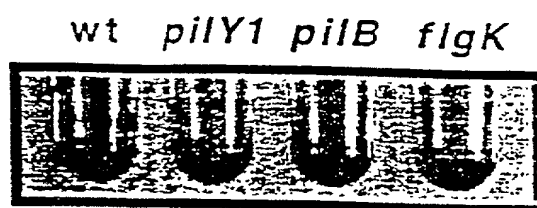


Fig. 16

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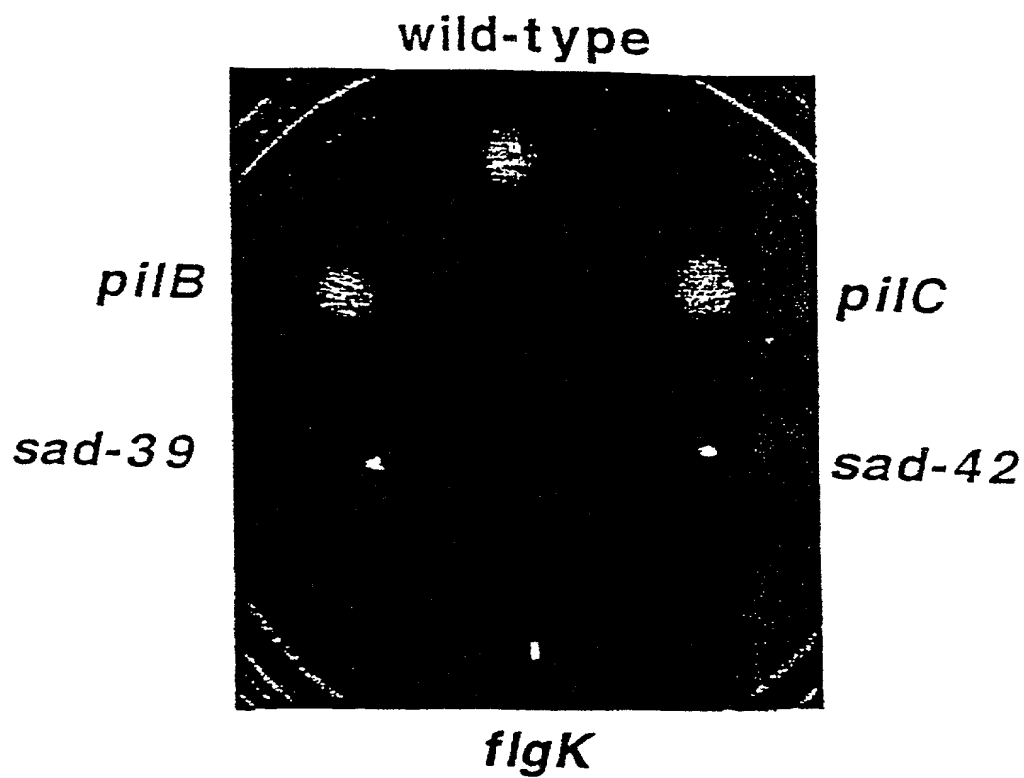


Fig. 17

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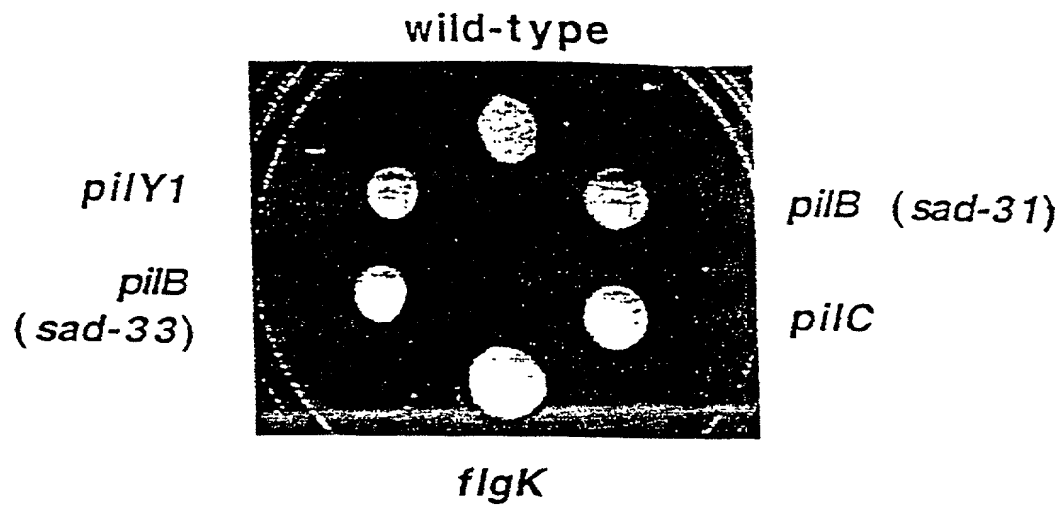


Fig. 18

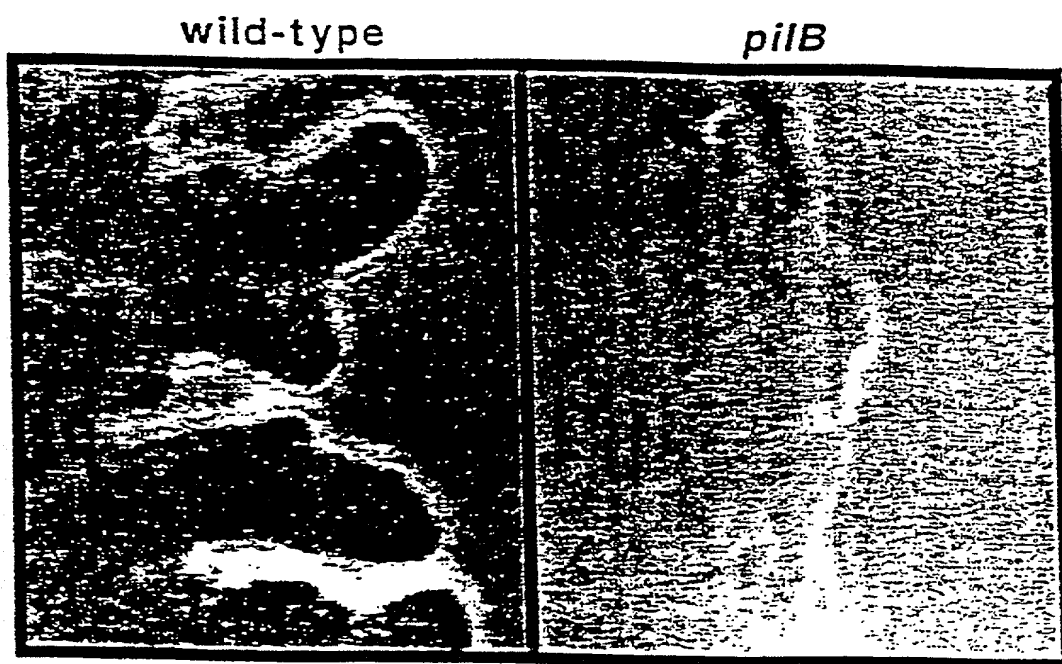


Fig.19

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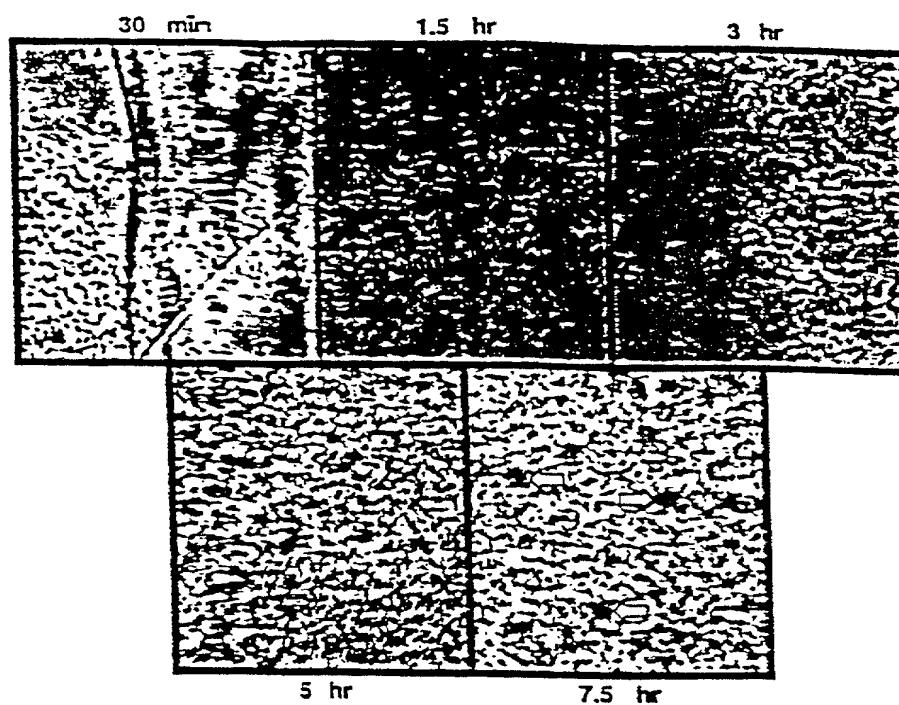


Fig. 20

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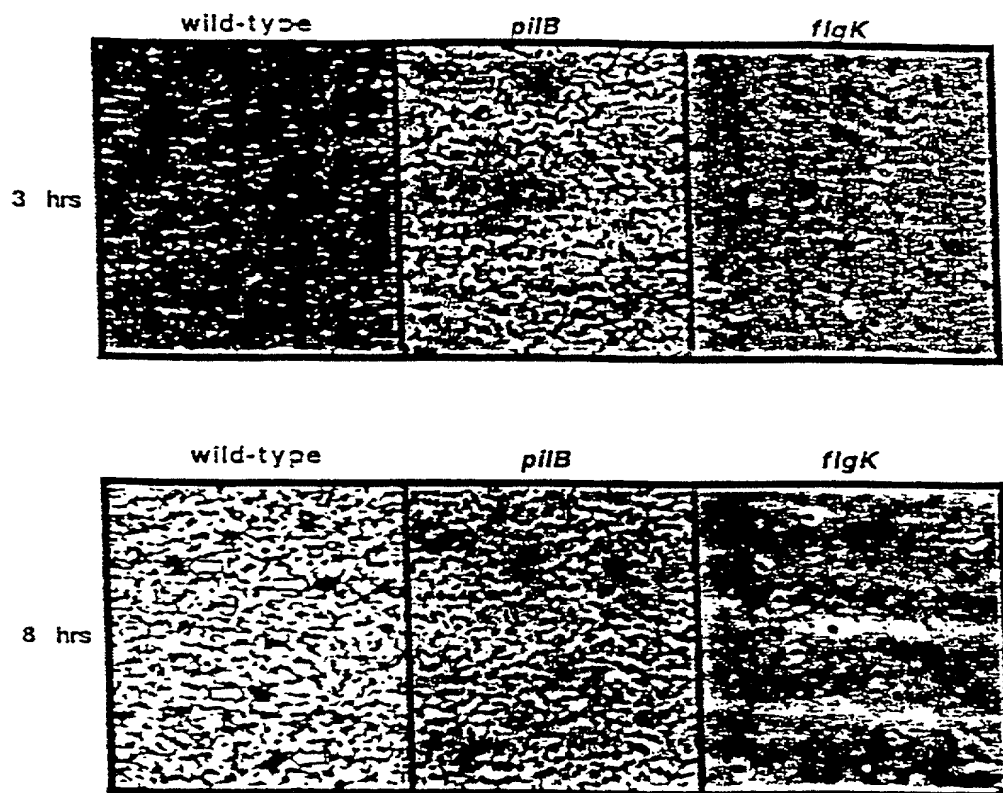


Fig. 21

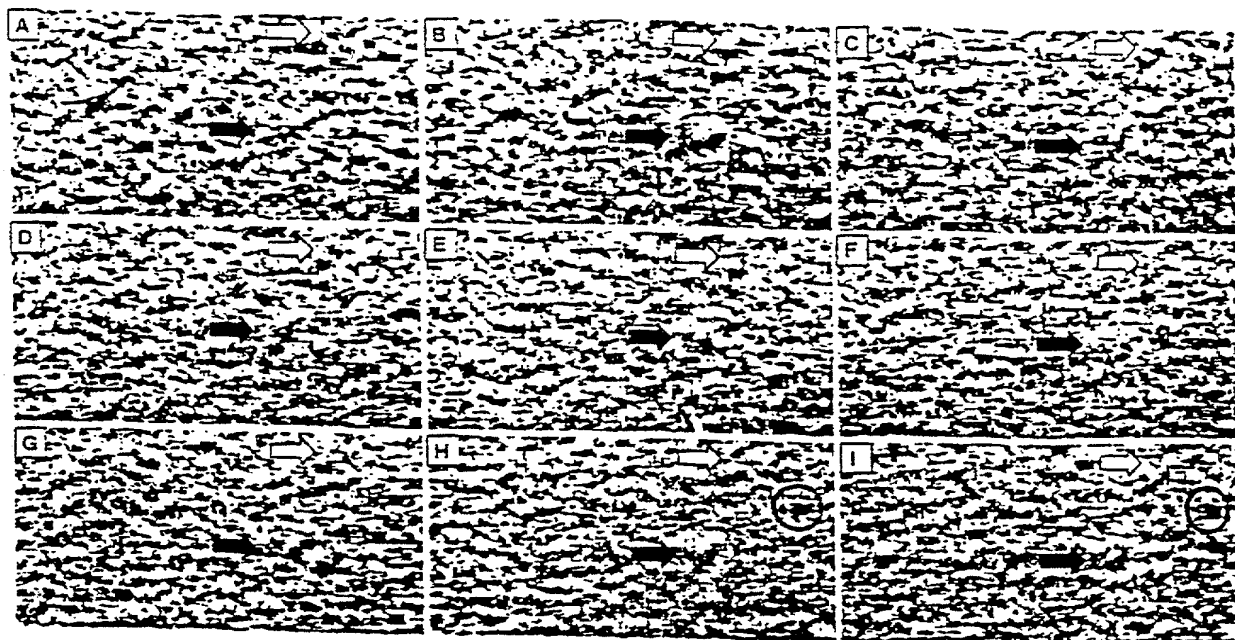


Fig. 22

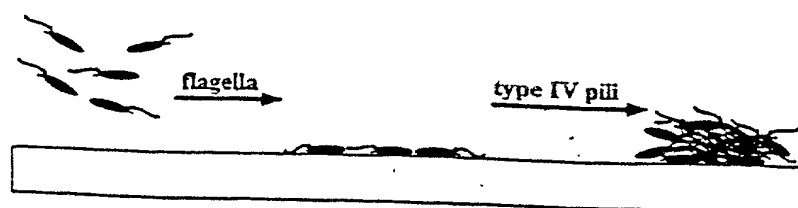


Fig. 23

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled REGULATION OF BIOFILM FORMATION, the specification of which

- ☐ is attached hereto.
☒ was filed on October 17, 2000 as Application Serial No. 09/673,605
☐ was described and claimed in PCT International Application No. _____
filed on _____ and as amended under PCT Article 19 on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56(a).

FOREIGN PRIORITY RIGHTS: I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

Country	Serial Number	Filing Date	Priority Claimed?
PCT	PCT/US99/09034	27 April 1999	Yes

PROVISIONAL PRIORITY RIGHTS: I hereby claim priority benefits under Title 35, United States Code, §119(e) and §120 of any United States provisional patent application(s) listed below filed by an inventor or inventors on the same subject matter as the present application and having a filing date before that of the application(s) of which priority is claimed:

Serial Number	Filing Date	Status
60/083,259	27 April 1998	Abandoned
60/102,870	02 October 1998	Abandoned

NON-PROVISIONAL PRIORITY RIGHTS: I hereby claim the benefit under Title 35, United States Code, §120 of any United States application(s) listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose all information

COMBINED DECLARATION AND POWER OF ATTORNEY

I know to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56(a) which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Serial Number	Filing Date	Status

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Paul T. Clark, Reg. No. ~~30,162~~, Karen L. Elbing, Ph.D. Reg. No. ~~35,238~~, Kristina Bieker-Brady, Ph.D. Reg. No. ~~39,109~~, Susan M. Michaud, Ph.D. Reg. No. ~~42,885~~, James D. DeCamp, Ph.D., Reg. No. ~~43,580~~, Sean J. Edman, Reg. No. ~~42,506~~, Timothy J. Douros, Reg. No. 41,716 6)

Address all telephone calls to: Kristina Bieker-Brady, Ph.D. at 617/428-0200.

Address all correspondence to: Kristina Bieker-Brady, Ph.D. at Clark & Elbing LLP, 176 Federal Street, Boston, MA 02110.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Full Name (First, Middle, Last)	Residence Address (City, State, Country)	Post Office Address (Street, City, State, Country)	Citizenship
<u>George A. O'Toole</u>	<u>Hanover, NH</u> NH	5 Fletcher Circle Hanover, NH 03755	United States
Signature: <u>George O'Toole</u>			Date: <u>12/11/01</u>

Full Name (First, Middle, Last)	Residence Address (City, State, Country)	Post Office Address (Street, City, State, Country)	Citizenship
<u>Roberto Kolter</u>	<u>Chestnut Hill, MA</u> MA	741 Heath Street #3 Chestnut Hill, MA 02467	United States
Signature: <u>RLK16</u>			Date: <u>12/5/01</u>

COMBINED DECLARATION AND POWER OF ATTORNEY

Full Name (First, Middle, Last)	Residence Address (City, State, Country)	Post Office Address (Street, City, State, Country)	Citizenship
Leslie A. Pratt	Belmont, MA MA	85 Elm Street Belmont, MA 02478	United States
Signature: <i>Leslie Pratt</i>			Date: 12/21/01

SEQUENCE LISTING

<110> The President and Fellows of Harvard College

<120> REGULATION OF BIOFILM FORMATION

<130> 00246/505WO3

<150> 60/102,870

<151> 1998-10-02

<150> 60/083,259

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nggtgttnna	accncggnc	cncttccgg	ccaangngng	aaatttncng	gtgggnggaa	600
aanaggtcna	ngttttnaan	gggtttccng	tnancntcnt	nnccccnan	ggntttnttn	660
ntnanaaacc	aaanntcncc	ngaatttnc	nccnggtngg	ntttttnncng	nannnnnggaa	720
nttnnnnggt	gggnnnnccn	ntcctttgtt	tnnaaaatna	nnctttttng	ggncnnnnnc	780
naaaagggnc	annngnggnc	cnnntggggn	ggnnnccnnn	gggnccnaag	nt	832

<210> 5

<211> 1054

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(1054)

<223> n is a, t, c, or g.

<400> 5

cncaanggc	cagagcacag	gatatgcngc	aatctcatgg	acaaacggcg	ccagcccnat	60
ggaggccacc	gacnccacat	cgtcgcgccc	ggtegttgc	aggcncgcca	acgcancctc	120
aagggtctgc	gccanttgca	ncnctnctc	gcnaccanc	cnnagttgcc	agcncncaa	180
actccccacc	ncnaanncnc	ntnacnaaat	nntgggtttc	cgnataccgc	ccnactcac	240
gcaccaattg	ctcaccncg	gcctgaacna	actggtcgg	ncnctncccg	ccccatccnc	300
tggttnaaac	nggcenattc	cttnaccccc	agcaacancn	aataaccggg	acctggccan	360
cnccgggtng	ctcaccggg	cattaaactg	cattttcaaa	atatnnccgg	ttggccacgc	420
cgtagnaggt	gtcctgntag	gacnccaccc	ccantttcnc	tntgccccn	ggngctgntcn	480
nggaannngn	ccntgagctt	tctcgaccat	ctgggtttct	tntctntgcn	cccactcncg	540
nnncaagttt	taaggtnttn	ntccgggna	atcctctnng	gcnannnctt	naactgnaaa	600
cttcnccga	acngggncct	aanantagnc	ctatnngggg	nnacnngcgt	tgncacaaccn	660
aactnttttt	ttttcccagc	cgcggggctn	ttcaagtctn	tgaacgnaac	tcctcnngtc	720
ntccacang	gnctcccccc	tantntntaa	ccgctntcn	tctatnttgg	gngtccccgn	780
ntncatacat	gnngagtan	aagaagctcn	ancctccna	nnnggntctc	cgccccccaa	840
ttntccccct	ctctcccttt	nancntctaa	atatattctt	tnntgggnnt	naanaagggg	900
ggcgcanaaa	nacntntctc	cggggggggt	tgtgggnctt	nnanaaaccc	ccctttctnt	960
tntnncccc	cctccgnggg	ggctcncccc	tcctnttttg	ttttccccnc	ctannaatcc	1020
ctactcncng	gnctagttga	aaaaacanna	acgc			1054

<210> 6

<211> 880

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(880)

<223> n is a, t, c, or g.

<400> 6

ncnnacgnnt	ngnaagtgat	caggccnatt	aaacnnntga	cnaaannaga	acangnnnggt	60
ctgttactac	tcttcaagac	caacccaagn	cgaccgtgna	tagcgngncc	tntacgcagc	120
atcngttccn	catttagatt	nnatccatc	cnaagtttc	nccgggtcag	aacgntnctt	180
gacgtacaac	ccatannngc	gggtannngg	nnatttttng	ctacctcnca	tgttttggaa	240
gnccnantnc	cnntaatng	gnagcnncan	ncangcnenn	ggggattatt	acnactcnac	300

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centgganaa cnttgccact acngcnggnc ccccgcnngn tccnggnctc cctgcccac      360
ttcccttgtc tcccgncctc tntnccccct tttcnegtcn ncttctgggtg tncgnttccc      420
ctccccccng tctctnttca ncnctngcg tctngggcac ctngncgnnc tcttccctnc      480
tgccccctct nccccctt cgttntancc cctctctcna cntncttcat cccgtccctn      540
ttcttntctt cncctncncc cctnttcta ntctntctgt cccnctncgn tcntcgctn      600
cctnncnccn ttntcgactt cncntgttg nccccccgc ngngncttct ctngtcttct      660
cccgtcngcn gctcagnncc cntccttccn ttntctntnn ctgtccgncn gcgnnctgt      720
ncctncgncc cctagnnngg ncgcgcctcn gcnnctctgt cccnngntnt nntctttctg      780
cncgtgtctc nntnttctn tntcnctcg cccatccnct nctctntnn nncgtngntt      840
cnccttctag gncnnattc cnannnngg cctttncccc      880

```

<210> 7

<211> 779

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(779)

<223> n is a, t, c, or g.

<400> 7

```

ncaanncaga tcctgnaaaa cgggaaaggt tccnttcagg tacgtactt gtgtataaaa      60
gtcagggccc aaacgcccc ggtgcaacaa ctggtcnaag gctacntggc gggttacaac      120
cgtgcgctgg tchnacgcaa ggccaaaggc ctgcccnaac aatgtgccag cnaatgggta      180
cggccgatca cggcgctgga cctgggtcaag ttgaccgcc ggctggttgt ggaagggggc      240
gtcggccagt tcgccnangc cctggcgccg gcgcaaccgc cccaggcnac cgcactcgcg      300
ggcaccgccg tcaccggttt cgcggcgccg gcaaccgccg agcagcnttt tgccctgaaa      360
cgcggcaaca atgcnttggg ccateggcan cnaacgctcg ttcaatgggc cgttnggaat      420
ntttgcttgg caaaccccc atttttcccg ttgggttagg cggcattcct tttctnacca      480
naaagcacct gaaccattcc cgggcaanct tgaaaattct tgggccccng ngcctgccaa      540
ttttgccnaa aaatcaanat cggtttcaac canccnctt gcctggaacc aaaccgtcaa      600
aaactccaaa aaaattcccc cttncnctt gcaatcnntc naagaaccaa cctttttttn      660
ccaaggnatt ttttttcna naaacnncaa angntttnt naattttacn acttaaggcc      720
anttnnaaag tncccaattt tttanngtcc aatttgnccc nattttaaag gctccggtt      779

```

<210> 8

<211> 848

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(848)

<223> n is a, t, c, or g.

<400> 8

```

gccnnnnncn nattatncaa gntctaagtg ttnnaccana tnccaaggac ataatgactt      60
ncctttatta antgtccgga ccatnccata tncaaccgtg canaccgtna acttnacca      120
ncatgntccc gcntgtcgta tttatanncc ccataagctt cncctgtcag aacgttncaa      180
taggtacant natactgcn ggcnatggc attttggtt tctttatgtt nggnagttcn      240
aacagccttt ttatggagcg tccacagcta tagggggaaa ntctattca acnctggcna      300
aantttgaaa aactnaganc tcnnnnggtt tataggggta tccntgacc aaannccnct      360
aattccnacb ctttgnctcc acttccctcc tngcgcnct ttaccnngg ccccgctcct      420
tcccnccngn ncntnggnca cngggggaaa ngnnntcncc cctggtttt ctccngtcn      480

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tnngnnnnncc	tcgtgnntcc	cggnncccttn	ccccccngtt	cggaactntt	ctccccctnch	540
cccnegcgng	tcgtctnnn	tnnccnngn	tnnccnggt	tnnccngcn	ccntttctc	600
ccccccccc	ttancngga	nccctctcc	tnccngtgc	cngcccccn	ggccccctcc	660
ctntnccctc	ggngnccnc	gnccnctcc	ttnncttgc	cctccctcn	ccntcnctc	720
cncctntcc	ntcccncc	ctntnnntc	ccccctgcc	nnnncccg	ccnttcgntc	780
ctnnnnnnn	tnccctngcc	cgcgtgcnc	gtngcgncc	gctntctgc	ctgtcncccc	840
ccctnccc						848

<210> 9

<211> 533

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(533)

<223> n is a, t, c, or g.

<400> 9

tatttggtga	taagntcagc	gccagcagtg	accgatgtca	cggataccat	cgacaccagc	60
accgtttcgc	tcacagcgac	ttcgacgggtg	gccgaagggtg	ggactgtcgt	ttacaccgcc	120
tcgggttaacg	cacccgtgac	cgacgctccg	ttgggttatca	ccctgttcca	aacggccana	180
ccatcnccat	tcgggttggn	gccagcancn	gcaccgtgaa	cttcgtgaca	ccaaacgacg	240
ccctcgcggg	cggcgataac	ctgagcgtga	agattgatga	cggcaagggt	ggcaattacn	300
aaaaactgga	catcgacgcc	accccgggcg	acaccaccgt	taccgatntg	caggacacta	360
cgggcctgac	cttgantgca	accgatagcg	ttgctgaang	cggntcgatc	gtttacaccg	420
caacattgac	caacgcnc	ggntcgccgt	tcnctgtnac	cctgaacaac	ngngcggtga	480
tcaacatccc	tgcgnggtt	cccccccg	tnctantcta	cacgngngaa	aaa	533

<210> 10

<211> 591

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(591)

<223> n is a, t, c, or g.

<400> 10

tgatttggtga	taagatcagc	cagcaaggcg	cgtcgctcgg	gttggttaaag	ccccaccagc	60
aacttgcca	gggaactctt	gcccagagccg	ctgcggccaa	tgatgccnat	tttctcgccc	120
ggcttganc	ccaggttnat	attctacacc	tngggnttct	gctgggtcgg	anaaatnaaa	180
nttcaactna	nngnattcca	acggccccctt	ccagaacttt	cnggtcangg	ggngctcntc	240
caaattgcgc	tcttggggca	gtccntcat	ctggctgana	ganatcttgg	tcaccccccc	300
ctggttggtat	cgggtcntca	ngcccnacaa	cnaaaccaac	nggctgaggg	cgcgaccgct	360
gaacatntnt	cangcgacca	ncccaccnt	gtcangcna	cggcgatna	tcaagtntac	420
nccnaaaana	anatgaccac	cccngccagt	tnctggatca	acaaagtgat	gttctttgcc	480
nggcgggana	acatcttcac	ccccanttct	aagcggtga	aggtgccgat	agtctgttcc	540
cncgtgtatt	ggcgtncnc	ccccntact	antcaacnch	tggnaaaaaa	a	591

<210> 11

<211> 1249

<212> DNA

<213> *Psuedomonas fluorescens*

<220>
 <221> variation
 <222> (1)...(1249)
 <223> n is a, t, c, or g.

<400> 11

ctgggtgtat aagatcaggg ccantngtgt cctggagtgt ctgtnacagt ggtttcggca	60
ngcttgccct cnanatncan tttttcgtaa ttgccaccct atggcctnct ccnaatttga	120
ancacnagnn acctnccan tgncaagggc ttcttcngcn tcnngaaatt canccnacnn	180
naaatngggc caaccctgan tggttaccgt cntgccgcnc ccnctcnggn catttctctg	240
ccnaagctc cgggtncctn gnttgccctc taaccaagc gncngntntn nancnncctt	300
gtttcncccc tncngncna cgggtggaan ggttttncce cntaggggc ctcnntntt	360
tctaaancgc ttttccagaa aaaggcctgc ccggtntacn ctttcttann tntcgtcgcg	420
tccnagngct tatcncctc tnncccttc ggatactnct ctgtaagttt ccctaaaatc	480
nnctggntng gnttctnnn anaaagaana tctntggggg cttntntnt tatatectct	540
cntattgtnc tttcnntan cntctntccn ngannctcat tcccganacc ctctnnnnnc	600
cgccttnenc tctctatan tttctnagtt gaaccgctcn tcccnctnca ctnttattnn	660
ntnngcgggn cgcnccttt gtccctcntt aacctgggg ntngcgagen tacnggctcn	720
ctccctaata ctctggggcg tnnngggcg nacgtcctcg ccttcgctcn naaatnnttc	780
ntaantcca acntcngcn gcccgcctc ggnnnnnnca atntntctc cccctattc	840
tngctacna gcngtgatn atcccttct cannagcctn ttcnggggat aacngngnag	900
ngannctctc tctttagtn cnaaancna tctctnctc tcttcttng gtcgcgctnc	960
tanancnctg gtcagttnn tctcnatgn nncnaggnt cccnnttnt cnetcnettc	1020
ttgnnnactc ccngtntgtc cnggantgg tcttcgcct cggnanennt gtcctntnt	1080
tencnanncg aanantctc ttnctaacac nccttcgcn aanacnttt nactctnccc	1140
tctccttctn ctntctcgtc tnatntnan ttnctnctc annngtgac tcgttagcnc	1200
tccgntcttt ccnantctc gcccctct cncnctcna nctatccc	1249

<210> 12
 <211> 373
 <212> DNA
 <213> Psuedomonas fluorescens

<220>
 <221> variation
 <222> (1)...(373)
 <223> n is a, t, c, or g.

<400> 12

tnattgtgta taagntcagg actagagntc ctctcttagt nacggttcgc agcgttttgc	60
accgcacgt ccantgcgn cccaccccg tactagtcga cacgtggana aactcgcccg	120
gagtcgacnc gtgggtanta gtcgaagcgt ggngangnt cncgntatna ggcntaan	180
ctgcatcacg aaagcngggg gaaggttctc naaaanttcn ccnatgaggg agaacacgga	240
aancccttta ccncagggg ggcccgaaa tctggcaacn gancggngg agaatcnncc	300
atttcgtcag ctccatgggc accaccggga acatcatggg cgtcnntnc cngtactant	360
cgaccgtggc caa	373

<210> 13
 <211> 683
 <212> DNA
 <213> Psuedomonas fluorescens

<220>
 <221> variation
 <222> (1)...(683)

<223> n is a, t, c, or g.

<400> 13

tgactgtgtg	ttataagntc	agncgcacnt	ggnagtcnc	ntntgggttg	tangatccgc	60
ancnattaag	ctggccnngg	gaaantcngg	ttcaaccggn	tgcnngcaat	ganncnntat	120
ttcactcncc	cggcgtnac	ncctnngtan	tantcgaccc	ntggncanta	ntantctaca	180
nntgggtcaaa	acntttcgan	nnngtaggng	ncgccctntn	tanangtnan	cttcgtnacg	240
ggggaggaaa	angctccccg	gnggccannn	gccgagccta	aaaaangagg	cangtanggg	300
tgngaaaaaa	naatanctng	atangacncc	acccnntttg	acgccaat	accgangtac	360
angaccnngn	cnaactcatt	ttnagtgtnc	gcgacagaaa	tttttanggn	cgcnccangn	420
gaanggtct	cnanggtttt	gnaaannnaa	acnaggccct	ccnntaaatg	gtggaccgcg	480
ggnaaanntt	nnccnecant	gggggtttga	aattactttt	caacaatctt	caaaacntcc	540
gggtcnancc	aggaggggnc	aaaaaaaaaa	tnttttcggn	gtngccnnaa	aaatatccna	600
aattttntcn	ccccccccc	nccnnaaaag	aaggnggggg	gggaagggga	aaaagggggg	660
aangaggggg	gggaaggggg	ggg				683

<210> 14

<211> 672

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(672)

<223> n is a, t, c, or g.

<400> 14

gtgcttgtgt	ataagntcag	nccctggcct	gngcgncnac	aactccggtn	nccgtctaca	60
ntttagcnaa	ggatcgggtc	ttgctngtc	tntctggntan	actnccggga	cnatccacct	120
caatactecn	nccattnacg	tctatggtaa	ccnggaggtc	ggtcancagn	ncnattaccg	180
gtntacacng	tggaaaacttc	gaaaatctng	tggcnaacac	gggacctgcg	gtccccncca	240
nttccgattc	ngngganacn	ncatggntgt	cncnnaacngg	nngcnacncc	attcctgnan	300
gggngccaan	ttcctttenc	ntcaanccgt	nggnaacggg	cccnaatncc	gtnaacgtta	360
ccnnnganaa	atggtcngtt	ttccattccc	ccgggggnan	aaaccgggac	ngaagatttc	420
aanaccgcg	cntntnattn	taccnngggg	nnngcgggtc	gncccccn	nnacnngtga	480
naangggggg	ctnttcaaan	ttcntngtgt	tnancaacnac	cctgggggtt	natantantt	540
ncanaattnc	gggnggaana	ccaccggggc	ttnannnctt	nnaacnggnc	nnncnacn	600
ctttccnnnn	ngggggggng	ttccnncnnc	ccccctttnn	nttnntttnn	aaannttttt	660
gggggaaaaa	aa					672

<210> 15

<211> 1676

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(1676)

<223> n is a, t, c, or g.

<400> 15

tgcttgtgta	taagatcagg	gcccgnccg	nccnnantta	ngtctgggtc	aacgacacnn	60
catnggtgcn	gtggnanctc	antttachag	gcnccttaaaa	ngcatnattg	ttatncagtn	120
ngncgaggtg	gntcctcccn	tanccgaagn	natntgnnna	cttgggaanga	tttnancntt	180
ttccantcgg	tngtaccag	nngtgantcn	tcantttctg	acaccnctg	gtnncnntcc	240


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tggtcacncc tanannngac cncctctctcc gntgnggggcc tggngcntaa tatnntaccg      300
gctttnnant gctgtcagta tnanctctcgn nagecngnaaa ntcnctctnc anncggtgtn      360
tntngtctcn cncctctcct nctcntacac tcnctnactn tntnctgnaa atcnntctnn      420
ctgtantatc acggncanctn cgttctntgt ggggctcnct tganaggctc cccctnacct      480
ctctannnac nggtgcgggt atnnncctat aanagctctg tgcagtntc acagtnacat      540
cgctgcnnnn cncngtagc tctgcacnt cgcctctttn tttctnttct ctengcaaan      600
atcttntnt ctctcnntcn atcattatc ncangecngg gggctctcct cccctcnnn      660
ncntcngttc nanacangtc ntntttagct atgtcttatg tncnctntc anttttntcn      720
cncctcnac ncttcagann ggctnngnct gacctctata gtcgntctc tccctcctct      780
nctnntctct cngcnataac gcnctnctc tcttggnctc tcnngctctc tnnntntata      840
tccnncgcn nttctctcta tctctcngt ntgtgctct caattgtncn ctctctcgt      900
cnnctgtcnn ntctanctn tcttgactt nannaatacn tacctctct ngcctctctn      960
cnnctnctct cncgcacat ctngaccgc tncctctcgn cngcgnatc tcttcttnc      1020
gttctcnnct tctcgcgct ctctnngtac tngcttttc cncctacnt ctctgctc      1080
ttcctcngt cncctcctc tctctctct ntctangtn ncnngcncat nggcttctc      1140
tcgctcnctn tcnctctct ntctnctcgt tctcgtctng atcnntctct catcatntc      1200
tntntntca tcanctntn tgncactct cnatctgtnt ctctntctta ntntcctc      1260
cttctnttc tcttanctn cgttnatnc nttctctgat nctctnagt atntctatgt      1320
acgctnnct tnatcngnn cctntctcta tcancatcat nctagctnnc ttcctatngt      1380
cctgctctca ctntttctgc cnanatatn atcnctnctc tntatctcn tanattntn      1440
cctntnaatg tttanaatg ctctactna nctctctn tctnnnctc cagntcactc      1500
tctanantg cctnngtta tacgntctn tncgcttan tgcgtntct atcantnng      1560
ctctttntt ctctctcnc ntgtntctn ncacactntc ttcctctct ctcnnatatn      1620
natgctnntc tatnnccnt tctatgctnt cncctntcna nccacantnt nntctc      1676

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<210> 16

<211> 721

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(721)

<223> n is a, t, c, or g.

<400> 16

```

tncctgtgta taagatcagg cctatngccg nctgnggntt ntctgggtgc ncgacgcgcc      60
attcgaaaaa ancagctccg nnaccngttc caantacacn nngttgtncn nccgnagtct      120
cagcttcngc ctgcenacg tnnacaattc ctncnaaac ctgggtgtgn tntccnnna      180
gctnatgtan ganngctnat nggctggnn gnactgtct accnagnctc angtnngcac      240
caaccngagc ntcattcng cnnacnnga acccngng nctgcttct ntcnaacnc      300
cnncaantcc aacnccatng gttgtgtgn cnacgacng ngcgaaaacn ncgncacnn      360
ngnccnagtc aagttccgc ataccacag cnggtcnggg ggtntcnccc cctntctgt      420
tccaaacatn nccatanaan nnnnggtntg ctgggggaat ccaancntc nnctgnggtt      480
cgatcnaaac aanatanggg tcaangnctn gccactgcn tnatnaattt cncagtgcc      540
cnnctnctn tgatnngcna agcnnncnn ggggtgngg gggnnnttnc cnnntatna      600
antanaaacg gcngntcct tnnccnccan ggggtgntgn ngnttttnaa aacnctttt      660
nnnnaaan ccccccncct ntttncnng gannannatc cnaaaannnn gtcccnccc      720
c

```

<210> 17

<211> 452

<212> DNA

<213> *Psuedomonas fluorescens*

<220>
 <221> variation
 <222> (1)...(452)
 <223> n is a, t, c, or g.

<400> 17
 atnnngnnnn tncctgtgta taagntcagg gcncncctn tcnaaacttn gtctgggtcg 60
 ngctacacnn cannggnnac tggcagctcg gtnaccgcta cctnanaacg cttcantgtt 120
 cctcagcngg tccacgtcca gccttgagcc acatgtnaaa annngccna caancnngg 180
 ngtnaanntc caggnntgc ncgacgantg ccaatnnaan nttctcnacn gtttcacctg 240
 gaangacctt gccganaccn anacnntcac caanggtgaa nncaactccc ggnagatnecg 300
 ctncacnccn gaccccaacg aatcctnccg cgngggtttt nttagcanca tcgncgncan 360
 caaccangnc canttcccc cgntntcatt ccnccnanc gacggnnntt ctgggcgtcn 420
 cccccccgt actantctac ncntnncaaa aa 452

<210> 18
 <211> 442
 <212> DNA
 <213> Psuedomonas fluorescens

<220>
 <221> variation
 <222> (1)...(422)
 <223> n is a, t, c, or g.

<400> 18
 tncctgtgta taagntcagg ntctnagatg agctcggtag ttcangagnt tttctgcgac 60
 cgcnnnccg acgntgnaa tcgntggcna ggtngcnta nacannnnaa agtanncccc 120
 tcgaancgnt cnntgacctc ctgntccaaa tngtcacngg cattggncga cgcngcnca 180
 ccnncactt cgctcgacnt cccaaaancn gcctgggccc ngcncgncng gattngccc 240
 gacatcnct nancaaantr cccnccgcn tactngncca nccttgacca nntttgenc 300
 tcctntcctt actgggtcng cttegnctcc ggnttgctna ccannatggt ccnaancctg 360
 ctgtctnca ctctcaaatn cgcccccggc caacntgct gatcgnettc nncnccnag 420
 tncatttcaa cccctgccca aa 442

<210> 19
 <211> 538
 <212> DNA
 <213> Psuedomonas fluorescens

<220>
 <221> variation
 <222> (1)...(538)
 <223> n is a, t, c, or g.

<400> 19
 ctttgttgta taagnatcag aactagagc ttgccccttc tncancnctt cnatggacag 60
 cggctttcgg gccgtcgagc aacgatctgt ccacagttna ncaccannag gcgntccacc 120
 atcaanagaa aggannncg gtnctnacc acnnacacan gtcttggtat cnaccacggc 180
 agccaagcgn tgtttcaaac gttcttcagc nggtgtgtcc atggatctgg ttggttcgtc 240
 caanaacaag ataggcgtgt tnanncnct ncnactngac acgtggaaat tntngctcta 300
 accncccgac angttctgtc nncnctncc naatnnnaat tcataacctt ncngatgccn 360
 gggggcaaat tcatnncnc ccgccanttc acggnctgga acacanttca actnncacgt 420
 ttnggcegcc naaaantctt gttgtcnccc aggnntttnn nancancnng atnttnttgg 480
 ggnnccttnc cnaantntt nnnennctcc cntnannttg aanntngnng gatgttna 538

<210> 20
 <211> 218
 <212> DNA
 <213> *Psuedomonas fluorescens*

<220>
 <221> variation
 <222> (1)...(218)
 <223> n is a, t, c, or g.

<400> 20
 tnatttgtgt ataagttcag gttgctngnt gnacgccatc ccggccaagg gttgccggcg 60
 tcacccacat ngtactagtc nncgcgtggc cnaaacgggtg angctctncta attgatgctt 120
 gccaacgntt naaaaaaaag tatngacagg gtnttaacca tcagnttntn ccnaaangta 180
 ctagtctacc cgtggccana naantnnann nntggnc 218

<210> 21
 <211> 642
 <212> DNA
 <213> *Psuedomonas fluorescens*

<220>
 <221> variation
 <222> (1)...(642)
 <223> n is a, t, c, or g.

<400> 21
 tncittgtgt ataagntcag gccccggggt ancgncagta ngntngnca ncggtcctg 60
 caagctgncg gcgnanatec ngcgctncct cttntgcnt ctgaaatgca ttnccctcn 120
 atgagtcggc tgtcttcang gttnggntgg ttncacatc catcancttg ntctccnctg 180
 ttaccccngc ngtnncctgc cgcctctca gaccnggatn cccgtncanc accccctagt 240
 tctaanaacg taccangan aangaacacc cgctcgcggtg tgggcctact tcacctatcc 300
 tgccccggtg acgcccgttg atacaccaag gaaagtctac acnaaccctt tggcaaaatc 360
 ctgtntatcg tgcgaaaaan gatggatata ccgaaaaaat cgctatantg accccnante 420
 anggttnttg caacggaaaa ncnctncttc cctgctgttt tgtggaatat ctaccgactg 480
 ganacaggcc aatgcatgaa attactgaac tgaagggaca agcaaaaaac catccaanna 540
 actncaccaa cnanctggcc gagtnggttt naatccccgc gccggccaaa aaacgcengc 600
 attaannaan gcnggttggt tctntnctc gnnnaaanaa aa 642

<210> 22
 <211> 583
 <212> DNA
 <213> *Psuedomonas fluorescens*

<220>
 <221> variation
 <222> (1)...(583)
 <223> n is a, t, c, or g.

<400> 22
 tattgtgtat aagatcagnc cagcngtggc cntacagntg ggacaggcgg cgctcgcaagc 60
 ttccccctga gtgntgntcc agnmatanc agncntgnt gttataaaca aancacggnn 120
 atcgtataac nccgttcgtg acngcgtatc gccanactn naatnccgna aacgggtnga 180
 aatccgtaat ccaagtgtta tcntgncgg gatgttctag agcaactcca tcatctntac 240
 aancttggtc gancttggtc tggcacctcc actgagacaa cgggtgntctc aatagtcanc 300

```

acnccccctnn cccccnggga gganatntnt cncctggncc acnncnancan catctttaac 360
gnatatttct tntttatcag cccnnttggg taccnntgc gtcattgggt ggntgcagcg 420
acaacncccg gagaaancna tttnccttggg nggtctntcn atcatcngca ccncccccca 480
aattganaag gtcgcccnc nccnngagan acnntancc angtcggccn tcnnccangtg 540
cgtggcgtcc cccnccgtn ctantcnacc cttnccagnc caa 583

```

<210> 23

<211> 360

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(360)

<223> n is a, t, c, or g.

<400> 23

```

tctttaanta gnaccgacga ntctctctan caccctaac cagtcnacgg ctngtggcga 60
ctggatatng aactngacc aggtcggggc ntccccac nntnctatt caacgcttgg 120
ccaaacacgt ggtcanatct ctncacagtg cccctctan cnttctcga tacactntc 180
ttcttccaat atccccgct aatccccctc catcngtgaa nnggccccgc tccattaaaa 240
agcatngngc mnacaaacaa ccngagatcn ttcnnttnn canncctccc gntccctcaa 300
atttcgnnag gggncgggtt ggcacccnaa accgntccn ngnggnaaat ttcttncntt 360

```

<210> 24

<211> 494

<212> DNA

<213> *Psuedomonas fluorescens*

<220>

<221> variation

<222> (1)...(494)

<223> n is a, t, c, or g.

<400> 24

```

tntttgtgta taagntcagg cgcaggcgng accgcactan ctatgtgang ngctctcngt 60
cggngnnnca ggcnatgccc gtcattgtcc atntgcngac naccctacta ctcttntgcn 120
tgancatgac tgccggggcg anaagttgcg cattgtcacc taaccctggg cgcctgtatg 180
tctncnaaaa naactgcaag atgctgggcc tggactacna aaccacggcc atcgtgttca 240
agcnctggg tntcgacgtg gaatggcagt tctgcccgtg gaancgctgc ctggtgatgc 300
tggancaggg gttggcgtag cgnnccngt acnnttnnac cntggnnaa ancnatncn 360
tgcngcttta cccnncnaa ncncntcng acntggaatt tgtgatnttc tacnccnatg 420
ccngcccca tcntttcgc ncnncnata anctgggngn cccncccccc gtnntantcn 480
accntgggna anaa 494

```

<210> 25

<211> 23

<212> DNA

<213> *Escherichia coli*

<400> 25

```

gaacgttacc atgtaggag gtc 23

```

<210> 26

<211> 35

<212> DNA
 <213> Artificial Sequence

<220>
 <221> variation
 <222> (1)...(35)
 <223> n is a, t, c, or g.

<223> Random sequence

<400> 26
 ggccacgcgt cgactagtagt nnnnnnnnnnn gatat 35

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Random sequence

<400> 27
 ggccacgcgt cgactagtagt 20

<210> 28
 <211> 24
 <212> DNA
 <213> Escherichia coli

<400> 28
 cgaggaaaggt tccgttcagg acgc 24

<210> 29
 <211> 35
 <212> DNA
 <213> Escherichia coli

<220>
 <221> variation
 <222> (1)...(35)
 <223> n is a, t, c, or g.

<400> 29
 ggccacgcgt cgactagtagt nnnnnnnnnnn acgcc 35

<210> 30
 <211> 17
 <212> DNA
 <213> Escherichia coli

<400> 30
 caggctctcc cgtggag 17

<210> 31
 <211> 17

<212> DNA

<213> Escherichia coli

<400> 31

ctgcctccca gagcctg

17

<210> 32

<211> 23

<212> DNA

<213> Escherichia coli

<400> 32

gcttccttta gcagcccttg cgc

23

<210> 33

<211> 24

<212> DNA

<213> Escherichia coli

<400> 33

cttccatgtg acctcctaac atgg

24

<210> 34

<211> 595

<212> PRT

<213> Escherichia coli

<400> 34

Met	Ala	Gln	Val	Ile	Asn	Thr	Asn	Ser	Leu	Ser	Leu	Ile	Thr	Gln	Asn
1				5					10					15	
Asn	Ile	Asn	Lys	Asn	Gln	Ser	Ala	Leu	Ser	Ser	Ser	Ile	Glu	Arg	Leu
		20						25				30			
Ser	Ser	Gly	Leu	Arg	Ile	Asn	Ser	Ala	Lys	Asp	Asp	Ala	Ala	Gly	Gln
		35				40					45				
Ala	Ile	Ala	Asn	Arg	Phe	Thr	Ser	Asn	Ile	Lys	Gly	Leu	Thr	Gln	Ala
	50					55					60				
Ala	Arg	Asn	Ala	Asn	Asp	Gly	Ile	Ser	Val	Ala	Gln	Thr	Thr	Glu	Gly
65				70					75					80	
Ala	Leu	Ser	Glu	Ile	Asn	Asn	Asn	Leu	Gln	Arg	Ile	Arg	Glu	Leu	Thr
			85					90					95		
Val	Gln	Ala	Ser	Thr	Gly	Thr	Asn	Ser	Asp	Ser	Asp	Leu	Asp	Ser	Ile
		100						105				110			
Gln	Asp	Glu	Ile	Lys	Ser	Arg	Leu	Asp	Glu	Ile	Asp	Arg	Val	Ser	Gly
		115				120					125				
Gln	Thr	Gln	Phe	Asn	Gly	Val	Asn	Val	Leu	Ala	Lys	Asp	Gly	Ser	Met
	130				135						140				
Lys	Ile	Gln	Val	Gly	Ala	Asn	Asp	Gly	Gln	Thr	Ile	Thr	Ile	Asp	Leu
145				150						155				160	
Lys	Lys	Ile	Asp	Ser	Asp	Thr	Leu	Gly	Leu	Asn	Gly	Phe	Asn	Val	Asn
			165					170					175		
Gly	Ser	Gly	Thr	Ile	Ala	Asn	Lys	Ala	Ala	Thr	Ile	Ser	Asp	Leu	Thr
		180					185					190			
Ala	Ala	Lys	Met	Asp	Ala	Ala	Thr	Asn	Thr	Ile	Thr	Thr	Thr	Asn	Asn
	195						200					205			
Ala	Leu	Thr	Ala	Ser	Lys	Ala	Leu	Asp	Gln	Leu	Lys	Asp	Gly	Asp	Thr

210 215 220
 Val Thr Ile Lys Ala Asp Ala Ala Gln Thr Ala Thr Val Tyr Thr Tyr
 225 230 235 240
 Asn Ala Ser Ala Gly Asn Phe Ser Phe Ser Asn Val Ser Asn Asn Thr
 245 250 255
 Ser Ala Lys Ala Gly Asp Val Ala Ala Ser Leu Leu Pro Pro Ala Gly
 260 265 270
 Gln Thr Ala Ser Gly Val Tyr Lys Ala Ala Ser Gly Glu Val Asn Phe
 275 280 285
 Asp Val Asp Ala Asn Gly Lys Ile Thr Ile Gly Gly Gln Glu Ala Tyr
 290 295 300
 Leu Thr Ser Asp Gly Asn Leu Thr Thr Asn Asp Ala Gly Gly Ala Thr
 305 310 315 320
 Ala Ala Thr Leu Asp Gly Leu Phe Lys Lys Ala Gly Asp Gly Gln Ser
 325 330 335
 Ile Gly Phe Asn Lys Thr Ala Ser Val Thr Met Gly Gly Thr Thr Tyr
 340 345 350
 Asn Phe Lys Thr Gly Ala Asp Ala Gly Ala Ala Thr Ala Asn Ala Gly
 355 360 365
 Val Ser Phe Thr Asp Thr Ala Ser Lys Glu Thr Val Leu Asn Lys Val
 370 375 380
 Ala Thr Ala Lys Gln Gly Thr Ala Val Ala Ala Asn Gly Asp Thr Ser
 385 390 395 400
 Ala Thr Ile Thr Tyr Lys Ser Gly Val Gln Thr Tyr Gln Ala Val Phe
 405 410 415
 Ala Ala Gly Asp Gly Thr Ala Ser Ala Lys Tyr Ala Asp Asn Thr Asp
 420 425 430
 Val Ser Asn Ala Thr Ala Thr Tyr Thr Asp Ala Asp Gly Glu Met Thr
 435 440 445
 Thr Ile Gly Ser Tyr Thr Thr Lys Tyr Ser Ile Asp Ala Asn Asn Gly
 450 455 460
 Lys Val Thr Val Asp Ser Gly Thr Gly Ser Gly Lys Tyr Ala Pro Lys
 465 470 475 480
 Val Gly Ala Glu Val Tyr Val Ser Ala Asn Gly Thr Leu Thr Thr Asp
 485 490 495
 Ala Thr Ser Glu Gly Thr Val Thr Lys Asp Pro Leu Lys Ala Leu Asp
 500 505 510
 Glu Ala Ile Ser Ser Ile Asp Lys Phe Arg Ser Ser Leu Gly Ala Ile
 515 520 525
 Gln Asn Arg Leu Asp Ser Ala Val Thr Asn Leu Asn Asn Thr Thr Thr
 530 535 540
 Asn Leu Ser Glu Ala Gln Ser Arg Ile Gln Asp Ala Asp Tyr Ala Thr
 545 550 555 560
 Glu Val Ser Asn Met Ser Lys Ala Gln Ile Ile Gln Gln Ala Gly Asn
 565 570 575
 Ser Val Leu Ala Lys Ala Asn Gln Val Pro Gln Gln Val Leu Ser Leu
 580 585 590
 Leu Gln Gly
 595

<210> 35

<211> 119

<212> PRT

<213> Escherichia coli

<400> 35
 Met Gly Ile Met His Thr Ser Glu Leu Leu Lys His Ile Tyr Asp Ile
 1 5 10 15
 Asn Leu Ser Tyr Leu Leu Leu Ala Gln Arg Leu Ile Val Gln Asp Lys
 20 25 30
 Ala Ser Ala Met Phe Arg Leu Gly Ile Asn Glu Glu Met Ala Thr Thr
 35 40 45
 Leu Ala Ala Leu Thr Leu Pro Gln Met Val Lys Leu Ala Glu Thr Asn
 50 55 60
 Gln Leu Val Cys His Phe Arg Phe Asp Ser His Gln Thr Ile Thr Gln
 65 70 75 80
 Leu Thr Gln Asp Ser Arg Val Asp Asp Leu Gln Gln Ile His Thr Gly
 85 90 95
 Ile Met Leu Ser Thr Arg Leu Leu Asn Asp Val Asn Gln Pro Glu Glu
 100 105 110
 Ala Leu Arg Lys Lys Arg Ala
 115

<210> 36

<211> 295

<212> PRT

<213> Escherichia coli

<400> 36
 Met Leu Ile Leu Leu Gly Tyr Leu Val Val Leu Gly Thr Val Phe Gly
 1 5 10 15
 Gly Tyr Leu Met Thr Gly Gly Ser Leu Gly Ala Leu Tyr Gln Pro Ala
 20 25 30
 Glu Leu Val Ile Ile Ala Gly Ala Gly Ile Gly Ser Phe Ile Val Gly
 35 40 45
 Asn Asn Gly Lys Ala Ile Lys Gly Thr Leu Lys Ala Leu Pro Leu Leu
 50 55 60
 Phe Arg Arg Ser Lys Tyr Thr Lys Ala Met Tyr Met Asp Leu Leu Ala
 65 70 75 80
 Leu Leu Tyr Arg Leu Met Ala Lys Ser Arg Gln Met Gly Met Phe Ser
 85 90 95
 Leu Glu Arg Asp Ile Glu Asn Pro Arg Glu Ser Glu Ile Phe Ala Ser
 100 105 110
 Tyr Pro Arg Ile Leu Ala Asp Ser Val Met Leu Asp Phe Ile Val Asp
 115 120 125
 Tyr Leu Arg Leu Ile Ile Ser Gly His Met Asn Thr Phe Glu Ile Glu
 130 135 140
 Ala Leu Met Asp Glu Glu Ile Glu Thr His Glu Ser Glu Ala Glu Val
 145 150 155 160
 Pro Ala Asn Ser Leu Ala Leu Val Gly Asp Ser Leu Pro Ala Phe Gly
 165 170 175
 Ile Val Ala Ala Val Met Gly Val Val His Ala Leu Gly Ser Ala Asp
 180 185 190
 Arg Pro Ala Ala Glu Leu Gly Ala Leu Ile Ala His Ala Met Val Gly
 195 200 205
 Thr Phe Leu Gly Ile Leu Leu Ala Tyr Gly Phe Ile Ser Pro Leu Ala
 210 215 220
 Thr Val Leu Arg Gln Lys Ser Ala Glu Thr Ser Lys Met Met Gln Cys
 225 230 235 240
 Val Lys Val Thr Leu Leu Ser Asn Leu Asn Gly Tyr Ala Pro Pro Ile


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<210> 37
<211> 308
<212> PRT
<213> Escherichia coli
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16

<210> 38
 <211> 245
 <212> PRT
 <213> Escherichia coli

<400> 38
 Met Arg Arg Leu Leu Ser Val Ala Pro Val Leu Leu Trp Leu Ile Thr
 1 5 10 15
 Pro Leu Ala Phe Ala Gln Leu Pro Gly Ile Thr Ser Gln Pro Leu Pro
 20 25 30
 Gly Gly Gly Gln Ser Trp Ser Leu Pro Val Gln Thr Leu Val Phe Ile
 35 40 45
 Thr Ser Leu Thr Phe Ile Pro Ala Ile Leu Leu Met Thr Ser Phe
 50 55 60
 Thr Arg Ile Ile Ile Val Phe Gly Leu Leu Arg Asn Ala Leu Gly Thr
 65 70 75 80
 Pro Ser Ala Pro Pro Asn Gln Val Leu Leu Gly Leu Ala Leu Phe Leu
 85 90 95
 Thr Phe Phe Ile Met Ser Pro Val Ile Asp Lys Ile Tyr Val Asp Ala
 100 105 110
 Tyr Gln Pro Phe Ser Glu Glu Lys Ile Ser Met Gln Glu Ala Leu Glu
 115 120 125
 Lys Gly Ala Gln Pro Leu Arg Glu Phe Met Leu Arg Gln Thr Arg Glu
 130 135 140
 Ala Asp Leu Gly Leu Phe Ala Arg Leu Ala Asn Thr Gly Pro Leu Gln
 145 150 155 160
 Gly Pro Glu Ala Val Pro Met Arg Ile Leu Leu Pro Ala Tyr Val Thr
 165 170 175
 Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Thr Ile Phe Ile Pro
 180 185 190
 Phe Leu Ile Ile Asp Leu Val Ile Ala Ser Val Leu Met Ala Leu Gly
 195 200 205
 Met Met Met Val Pro Pro Ala Thr Ile Ala Leu Pro Phe Lys Leu Met
 210 215 220
 Leu Phe Val Leu Val Asp Gly Trp Gln Leu Leu Val Gly Ser Leu Ala
 225 230 235 240
 Gln Ser Phe Tyr Ser
 245

<210> 39
 <211> 375
 <212> PRT
 <213> Escherichia coli

<400> 39
 Met Ile Arg Leu Ala Pro Leu Ile Thr Ala Asp Val Asp Thr Thr Thr
 1 5 10 15
 Leu Pro Gly Gly Lys Ala Ser Asp Ala Ala Gln Asp Phe Leu Ala Leu
 20 25 30
 Leu Ser Glu Ala Leu Ala Gly Glu Thr Thr Thr Asp Lys Ala Ala Pro
 35 40 45
 Gln Leu Leu Val Ala Thr Asp Lys Pro Thr Thr Lys Gly Glu Pro Leu
 50 55 60
 Ile Ser Asp Ile Val Ser Asp Ala Gln Gln Ala Asn Leu Leu Ile Pro
 65 70 75 80

Val Asp Glu Thr Pro Pro Val Ile Asn Asp Glu Gln Ser Thr Ser Thr
 85 90 95
 Pro Leu Thr Thr Ala Gln Thr Met Ala Leu Ala Ala Val Ala Asp Lys
 100 105 110
 Asn Thr Thr Lys Asp Glu Lys Ala Asp Asp Leu Asn Glu Asp Val Thr
 115 120 125
 Ala Ser Leu Ser Ala Leu Phe Ala Met Leu Pro Gly Phe Asp Asn Thr
 130 135 140
 Pro Lys Val Thr Asp Ala Pro Ser Thr Val Leu Pro Thr Glu Lys Pro
 145 150 155 160
 Thr Leu Phe Thr Lys Leu Thr Ser Glu Gln Leu Thr Thr Ala Gln Pro
 165 170 175
 Asp Asp Ala Pro Gly Thr Pro Ala Gln Pro Leu Thr Pro Leu Val Ala
 180 185 190
 Glu Ala Gln Ser Lys Ala Glu Val Ile Ser Thr Pro Ser Pro Val Thr
 195 200 205
 Ala Ala Ala Ser Pro Leu Ile Thr Pro His Gln Thr Gln Pro Leu Pro
 210 215 220
 Thr Val Ala Ala Pro Val Leu Ser Ala Pro Leu Gly Ser His Glu Trp
 225 230 235 240
 Gln Gln Ser Leu Ser Gln His Ile Ser Leu Phe Thr Arg Gln Gly Gln
 245 250 255
 Gln Ser Ala Glu Leu Arg Leu His Pro Gln Asp Leu Gly Glu Val Gln
 260 265 270
 Ile Ser Leu Lys Val Asp Asp Asn Gln Ala Gln Ile Gln Met Val Ser
 275 280 285
 Pro His Gln His Val Arg Ala Ala Leu Glu Ala Ala Leu Pro Val Leu
 290 295 300
 Arg Thr Gln Leu Ala Glu Ser Gly Ile Gln Leu Gly Gln Ser Asn Ile
 305 310 315 320
 Ser Gly Glu Ser Phe Ser Gly Gln Gln Gln Ala Ala Ser Gln Gln Gln
 325 330 335
 Gln Ser Gln Arg Thr Ala Asn His Glu Pro Leu Ala Gly Glu Asp Asp
 340 345 350
 Asp Thr Leu Pro Val Pro Val Ser Leu Gln Gly Arg Val Thr Gly Asn
 355 360 365
 Ser Gly Val Asp Ile Phe Ala
 370 375

<210> 40

<211> 547

<212> PRT

<213> Escherichia coli

<400> 40

Met Ser Ser Leu Ile Asn Asn Ala Met Ser Gly Leu Asn Ala Ala Gln
 1 5 10 15
 Ala Ala Leu Asn Thr Ala Ser Asn Asn Ile Ser Ser Tyr Asn Val Ala
 20 25 30
 Gly Tyr Thr Arg Gln Thr Thr Ile Met Ala Gln Ala Asn Ser Thr Leu
 35 40 45
 Gly Ala Gly Gly Trp Val Gly Asn Gly Val Tyr Val Ser Gly Val Gln
 50 55 60
 Arg Glu Tyr Asp Ala Phe Ile Thr Asn Gln Leu Arg Ala Ala Gln Thr
 65 70 75 80

Gln Ser Ser Gly Leu Thr Ala Arg Tyr Glu Gln Met Ser Lys Ile Asp
 85 90 95
 Asn Met Leu Ser Thr Ser Thr Ser Ser Leu Ala Thr Gln Met Gln Asp
 100 105 110
 Phe Phe Thr Ser Leu Gln Thr Leu Val Ser Asn Ala Glu Asp Pro Ala
 115 120 125
 Ala Arg Gln Ala Leu Ile Gly Lys Ser Glu Gly Leu Val Asn Gln Phe
 130 135 140
 Lys Thr Thr Asp Gln Tyr Leu Arg Asp Gln Asp Lys Gln Val Asn Ile
 145 150 155 160
 Ala Ile Gly Ala Ser Val Asp Gln Ile Asn Asn Tyr Ala Lys Gln Ile
 165 170 175
 Ala Ser Leu Asn Asp Gln Ile Ser Arg Leu Thr Gly Val Gly Ala Gly
 180 185 190
 Ala Ser Pro Asn Asn Leu Leu Asp Gln Arg Asp Gln Leu Val Ser Glu
 195 200 205
 Leu Asn Gln Ile Val Gly Val Glu Val Ser Val Gln Asp Gly Gly Thr
 210 215 220
 Tyr Asn Ile Thr Met Ala Asn Gly Tyr Ser Leu Val Gln Gly Ser Thr
 225 230 235 240
 Ala Arg Gln Leu Ala Ala Val Pro Ser Ser Ala Asp Pro Ser Arg Thr
 245 250 255
 Thr Val Ala Tyr Val Asp Gly Thr Ala Gly Asn Ile Glu Ile Pro Glu
 260 265 270
 Lys Leu Leu Asn Thr Gly Ser Leu Gly Gly Ile Leu Thr Phe Arg Ser
 275 280 285
 Gln Asp Leu Asp Gln Thr Arg Asn Thr Leu Gly Gln Leu Ala Leu Ala
 290 295 300
 Phe Ala Glu Ala Phe Asn Thr Gln His Lys Ala Gly Phe Asp Ala Asn
 305 310 315 320
 Gly Asp Ala Gly Glu Asp Phe Phe Ala Ile Gly Lys Pro Ala Val Leu
 325 330 335
 Gln Asn Thr Lys Asn Lys Gly Asp Val Ala Ile Gly Ala Thr Val Thr
 340 345 350
 Asp Ala Ser Ala Val Leu Ala Thr Asp Tyr Lys Ile Ser Phe Asp Asn
 355 360 365
 Asn Gln Trp Gln Val Thr Arg Leu Ala Ser Asn Thr Thr Phe Thr Val
 370 375 380
 Thr Pro Asp Ala Asn Gly Lys Val Ala Phe Asp Gly Leu Glu Leu Thr
 385 390 395 400
 Phe Thr Gly Thr Pro Ala Val Asn Asp Ser Phe Thr Leu Lys Pro Val
 405 410 415
 Ser Asp Ala Ile Val Asn Met Asp Val Leu Ile Thr Asp Glu Ala Lys
 420 425 430
 Ile Ala Met Ala Ser Glu Glu Asp Ala Gly Asp Ser Asp Asn Arg Asn
 435 440 445
 Gly Gln Ala Leu Leu Asp Leu Gln Ser Asn Ser Lys Thr Val Gly Gly
 450 455 460
 Ala Lys Ser Phe Asn Asp Ala Tyr Ala Ser Leu Val Ser Asp Ile Gly
 465 470 475 480
 Asn Lys Thr Ala Thr Leu Lys Thr Ser Ser Ala Thr Gln Gly Asn Val
 485 490 495
 Val Thr Gln Leu Ser Asn Gln Gln Gln Ser Ile Ser Gly Val Asn Leu
 500 505 510
 Asp Glu Glu Tyr Gly Asn Leu Gln Arg Phe Gln Gln Tyr Tyr Leu Ala

515 520 525
 Asn Ala Gln Val Leu Gln Thr Ala Asn Ala Ile Phe Asp Ala Leu Ile
 530 535 540
 Asn Ile Arg
 545

<210> 41
 <211> 566
 <212> PRT
 <213> Psuedomonas aeruginosa

<400> 41
 Met Asn Asp Ser Ile Gln Leu Ser Gly Leu Ser Arg Gln Leu Val Gln
 1 5 10 15
 Ala Asn Leu Leu Asp Glu Lys Thr Ala Leu Gln Ala Gln Thr Gln Ala
 20 25 30
 Gln Arg Asn Lys Leu Ser Leu Val Thr His Leu Val Gln Asn Lys Leu
 35 40 45
 Val Ser Gly Leu Ala Leu Ala Glu Leu Ser Ala Glu Gln Phe Gly Ile
 50 55 60
 Ala Tyr Cys Asp Leu Asn Ser Leu Asp Arg Glu Ser Phe Pro Arg Asp
 65 70 75 80
 Ala Ile Ser Glu Lys Leu Val Arg Gln His Arg Val Ile Pro Leu Trp
 85 90 95
 Arg Arg Gly Asn Lys Leu Phe Val Gly Ile Ser Asp Ala Ala Asn His
 100 105 110
 Gln Ala Ile Asn Asp Val Gln Phe Ser Thr Gly Leu Thr Thr Glu Ala
 115 120 125
 Ile Leu Val Glu Asp Asp Lys Leu Gly Leu Ala Ile Asp Lys Leu Phe
 130 135 140
 Glu Asn Ala Thr Asp Gly Leu Ala Gly Leu Asp Asp Val Asp Leu Glu
 145 150 155 160
 Gly Leu Asp Val Gly Val Lys Glu Thr Ser Gly Gln Glu Asp Thr Gly
 165 170 175
 Ala Glu Ala Asp Asp Ala Pro Val Val Arg Phe Val Asn Lys Met Leu
 180 185 190
 Leu Asp Ala Ile Lys Gly Gly Ser Ser Asp Leu His Phe Glu Pro Tyr
 195 200 205
 Glu Lys Ile Tyr Arg Val Arg Phe Arg Thr Asp Gly Met Leu His Glu
 210 215 220
 Val Ala Lys Pro Pro Ile Gln Leu Ala Ser Arg Ile Ser Ala Arg Leu
 225 230 235 240
 Lys Val Met Ala Gly Leu Asp Ile Ser Glu Arg Arg Lys Pro Gln Asp
 245 250 255
 Gly Arg Ile Lys Met Arg Val Ser Lys Thr Lys Ser Ile Asp Phe Arg
 260 265 270
 Val Asn Thr Leu Pro Thr Leu Trp Gly Glu Lys Ile Val Met Arg Ile
 275 280 285
 Leu Asp Ser Ser Ser Ala Gln Met Gly Ile Asp Ala Leu Gly Tyr Glu
 290 295 300
 Glu Asp Gln Lys Glu Leu Tyr Leu Ala Ala Leu Lys Gln Pro Gln Gly
 305 310 315 320
 Met Ile Leu Val Thr Gly Pro Thr Gly Ser Gly Lys Thr Val Ser Leu
 325 330 335
 Tyr Thr Gly Leu Asn Ile Leu Asn Thr Thr Asp Ile Asn Ile Ser Thr

340 345 350
 Ala Glu Asp Pro Val Glu Ile Asn Leu Glu Gly Ile Asn Gln Val Asn
 355 360 365
 Val Asn Pro Arg Gln Gly Met Asp Phe Ser Gln Ala Leu Arg Ala Phe
 370 375 380
 Leu Arg Gln Asp Pro Asp Val Ile Met Val Gly Glu Ile Arg Asp Leu
 385 390 395 400
 Glu Thr Ala Glu Ile Ala Ile Lys Ala Ala Gln Thr Gly His Met Val
 405 410 415
 Met Ser Thr Leu His Thr Asn Ser Ala Ala Glu Thr Leu Thr Arg Leu
 420 425 430
 Leu Asn Met Gly Val Pro Ala Phe Asn Leu Ala Thr Ser Val Asn Leu
 435 440 445
 Ile Ile Ala Gln Arg Leu Ala Arg Lys Leu Cys Ser His Cys Lys Lys
 450 455 460
 Glu His Asp Val Pro Lys Glu Thr Leu Leu His Glu Gly Phe Pro Glu
 465 470 475 480
 Glu Leu Ile Gly Thr Phe Lys Leu Tyr Ser Pro Val Gly Cys Asp His
 485 490 495
 Cys Lys Asn Gly Tyr Lys Gly Arg Val Gly Ile Tyr Glu Val Val Lys
 500 505 510
 Asn Thr Pro Ala Leu Gln Arg Ile Ile Met Glu Glu Gly Asn Ser Ile
 515 520 525
 Glu Ile Ala Glu Gln Ala Arg Lys Glu Gly Phe Asn Asp Leu Arg Thr
 530 535 540
 Ser Gly Leu Leu Lys Ala Met Gln Gly Ile Thr Ser Leu Glu Glu Val
 545 550 555 560
 Asn Arg Val Thr Lys Asp
 565

<210> 42

<211> 406

<212> PRT

<213> *Psuedomonas aeruginosa*

<400> 42

Met Ala Asp Lys Ala Leu Lys Thr Ser Val Phe Ile Trp Glu Gly Thr
 1 5 10 15
 Asp Lys Lys Gly Ala Lys Val Lys Gly Glu Leu Thr Gly Gln Asn Pro
 20 25 30
 Met Leu Val Lys Ala His Leu Arg Lys Gln Gly Ile Asn Pro Leu Lys
 35 40 45
 Val Arg Lys Lys Gly Ile Ser Leu Leu Gly Ala Gly Lys Lys Val Lys
 50 55 60
 Pro Met Asp Ile Ala Leu Phe Thr Arg Gln Met Ala Thr Met Met Gly
 65 70 75 80
 Ala Gly Val Pro Leu Gln Ser Phe Asp Ile Ile Gly Glu Gly Phe
 85 90 95
 Asp Asn Pro Asn Met Arg Lys Leu Val Asp Glu Ile Lys Gln Glu Val
 100 105 110
 Ser Ser Gly Asn Ser Leu Ala Asn Ser Leu Arg Lys Lys Pro Gln Tyr
 115 120 125
 Phe Asp Glu Leu Tyr Cys Asn Leu Val Asp Ala Gly Glu Gln Ser Gly
 130 135 140
 Ala Leu Glu Asn Leu Leu Asp Arg Val Ala Thr Tyr Lys Glu Lys Thr

145 150 155 160
 Glu Ser Leu Lys Ala Lys Ile Lys Lys Ala Met Thr Tyr Pro Ile Ala
 165 170 175
 Val Ile Ile Val Ala Leu Ile Val Ser Ala Ile Leu Leu Ile Lys Val
 180 185 190
 Val Pro Gln Phe Gln Ser Val Phe Glu Gly Phe Gly Ala Glu Leu Pro
 195 200 205
 Ala Phe Thr Gln Met Ile Val Asn Leu Ser Glu Phe Met Gln Glu Trp
 210 215 220
 Trp Phe Phe Ile Ile Leu Ala Ile Ala Ile Phe Gly Phe Ala Phe Lys
 225 230 235 240
 Glu Leu His Lys Arg Ser Gln Lys Phe Arg Asp Thr Leu Asp Arg Thr
 245 250 255
 Ile Leu Lys Leu Pro Ile Phe Gly Gly Ile Val Tyr Lys Ser Ala Val
 260 265 270
 Ala Arg Tyr Ala Arg Thr Leu Ser Thr Thr Phe Ala Ala Gly Val Pro
 275 280 285
 Leu Val Asp Ala Leu Asp Ser Val Ser Gly Ala Thr Gly Asn Ile Val
 290 295 300
 Phe Lys Asn Ala Val Ser Lys Ile Lys Gln Asp Val Ser Thr Gly Met
 305 310 315 320
 Gln Leu Asn Phe Ser Met Arg Thr Thr Ser Val Phe Pro Asn Met Ala
 325 330 335
 Ile Gln Met Thr Ala Ile Gly Glu Glu Ser Gly Ser Leu Asp Glu Met
 340 345 350
 Leu Ser Lys Val Ala Ser Tyr Tyr Glu Glu Glu Val Asp Asn Ala Val
 355 360 365
 Asp Asn Leu Thr Thr Leu Met Glu Pro Met Ile Met Ala Val Leu Gly
 370 375 380
 Val Leu Val Gly Gly Leu Ile Val Ala Met Tyr Leu Pro Ile Phe Gln
 385 390 395 400
 Leu Gly Asn Val Val Gly
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<210> 43

<211> 290

<212> PRT

<213> Psuedomonas aeruginosa

<400> 43

Met Pro Leu Leu Asp Tyr Leu Ala Ser His Pro Leu Ala Phe Val Leu
 1 5 10 15
 Cys Ala Ile Leu Leu Gly Leu Leu Val Gly Ser Phe Leu Asn Val Val
 20 25 30
 Val His Arg Leu Pro Lys Met Met Glu Arg Asn Trp Lys Ala Glu Ala
 35 40 45
 Arg Glu Ala Leu Gly Leu Glu Pro Glu Pro Lys Gln Ala Thr Tyr Asn
 50 55 60
 Leu Val Leu Pro Asn Ser Ala Cys Pro Arg Cys Gly His Glu Ile Arg
 65 70 75 80
 Pro Trp Glu Asn Ile Pro Leu Val Ser Tyr Leu Ala Leu Gly Gly Lys
 85 90 95
 Cys Ser Ser Cys Lys Ala Ala Ile Gly Lys Arg Tyr Pro Leu Val Glu
 100 105 110
 Leu Ala Thr Ala Leu Leu Ser Gly Tyr Val Ala Trp His Phe Gly Phe

115 120 125
 Thr Trp Gln Ala Gly Ala Met Leu Leu Leu Thr Trp Gly Leu Leu Ala
 130 135 140
 Met Ser Leu Ile Asp Ala Asp His Gln Leu Leu Pro Asp Val Leu Val
 145 150 155 160
 Leu Pro Leu Leu Trp Leu Gly Leu Ile Ala Asn His Phe Gly Leu Phe
 165 170 175
 Ala Ser Leu Asp Asp Ala Leu Phe Gly Ala Val Phe Gly Tyr Leu Ser
 180 185 190
 Leu Trp Ser Val Phe Trp Leu Phe Lys Leu Val Thr Gly Lys Glu Gly
 195 200 205
 Met Gly Tyr Gly Asp Phe Lys Leu Leu Ala Met Leu Gly Ala Trp Gly
 210 215 220
 Gly Trp Gln Ile Leu Pro Leu Thr Ile Leu Leu Ser Ser Leu Val Gly
 225 230 235 240
 Ala Ile Leu Gly Val Ile Met Leu Arg Leu Arg Asn Ala Glu Ser Gly
 245 250 255
 Thr Pro Ile Pro Phe Gly Pro Tyr Leu Ala Ile Ala Gly Trp Ile Ala
 260 265 270
 Leu Leu Trp Gly Asp Gln Ile Thr Arg Thr Tyr Leu Gln Phe Ala Gly
 275 280 285
 Phe Lys
 290

<210> 44

<211> 185

<212> PRT

<213> Psuedomonas aeruginosa

<400> 44

Met Leu Leu Lys Ser Arg His Arg Ser Leu His Gln Ser Gly Phe Ser
 1 5 10 15
 Met Ile Glu Val Leu Val Ala Leu Leu Ile Ser Ile Gly Val Leu
 20 25 30
 Gly Met Ile Ala Met Gln Gly Lys Thr Ile Gln Tyr Thr Ala Asp Ser
 35 40 45
 Val Glu Arg Asn Lys Ala Ala Met Leu Gly Ser Asn Leu Leu Glu Ser
 50 55 60
 Met Arg Ala Ser Pro Lys Ala Leu Tyr Asp Val Lys Asp Gln Met Ala
 65 70 75 80
 Thr Gln Ser Asp Phe Phe Lys Ala Lys Gly Ser Ala Phe Pro Thr Ala
 85 90 95
 Pro Ser Ser Cys Thr Pro Leu Pro Asp Ala Ile Lys Asp Arg Leu Gly
 100 105 110
 Cys Trp Ala Glu Gln Val Lys Asn Glu Leu Pro Gly Ala Gly Asp Leu
 115 120 125
 Leu Lys Ser Asp Tyr Tyr Ile Cys Arg Ser Ser Lys Pro Gly Asp Cys
 130 135 140
 Asp Gly Lys Gly Ser Met Leu Glu Ile Arg Leu Ala Trp Arg Gly Lys
 145 150 155 160
 Gln Gly Ala Cys Val Asn Ala Ala Asp Ser Ser Ala Asp Thr Ser Leu
 165 170 175
 Cys Tyr Tyr Thr Leu Arg Val Glu Pro
 180 185

<210> 45
 <211> 274
 <212> PRT
 <213> Psuedomonas aeruginosa

<400> 45
 Met Ser Met Asn Asn Arg Ser Arg Arg Gln Ser Gly Leu Ser Met Ile
 1 5 10 15
 Glu Leu Leu Val Ala Leu Ala Ile Ser Ser Phe Leu Ile Leu Gly Ile
 20 25 30
 Thr Gln Ile Tyr Leu Asp Asn Lys Arg Asn Tyr Leu Phe Gln Gln Gly
 35 40 45
 Gln Ala Gly Asn Gln Glu Asn Gly Arg Phe Ala Met Met Phe Leu Asp
 50 55 60
 Gln Gln Leu Ala Lys Val Gly Phe Arg Arg Arg Ala Asp Asp Pro Asn
 65 70 75 80
 Glu Phe Ala Phe Pro Ala Gln Gln Lys Thr Ala Tyr Cys Glu Ala Phe
 85 90 95
 Lys Ala Gly Ser Thr Leu Val Pro Ala Val Val Lys Ala Gly Gln Ser
 100 105 110
 Gly Phe Cys Tyr Arg Tyr Gln Pro Ala Pro Gly Glu Ala Tyr Asp Cys
 115 120 125
 Glu Gly Asn Ser Ile Thr Thr Pro Ser Asp Pro Phe Ala Thr Ala Gln
 130 135 140
 Ala Ile Thr Ala Arg Val Leu Phe Val Pro Ala Thr Ala Asp Val Pro
 145 150 155 160
 Gly Ser Leu Ala Cys Ser Ala Gln Thr Ile Lys Glu Lys Gly Gln Glu
 165 170 175
 Ile Val Ser Gly Leu Val Asp Phe Lys Leu Glu Tyr Gly Val Gly Pro
 180 185 190
 Thr Met Ala Gly Lys Arg Glu Val Glu Ser Phe Val Glu Gln Ala Asn
 195 200 205
 Ile Ala Asp Arg Pro Val Arg Ala Leu Arg Tyr Ser Ala Leu Met Ala
 210 215 220
 Ser Asp Lys Asn Leu Arg Gln Gly Asp Ser Lys Thr Leu Asp Asp Trp
 225 230 235 240
 Ile Thr Leu Tyr Pro Ser Ser Lys Thr Ser Leu Gln Gly Asn Asp Lys
 245 250 255
 Asp Arg Leu Tyr Gln Ile Ala Lys Gly Ser Gln Thr Leu Arg Asn Leu
 260 265 270
 Val Pro

<210> 46
 <211> 172
 <212> PRT
 <213> Psuedomonas aeruginosa

<400> 46
 Met Asn Asn Phe Pro Ala Gln Gln Arg Gly Ala Thr Leu Val Ile Ala
 1 5 10 15
 Leu Ala Ile Leu Val Ile Val Thr Leu Leu Ala Val Ser Ser Met Arg
 20 25 30
 Glu Val Val Leu Glu Ser Arg Ile Thr Gly Asn Val Ile Glu Gln Thr
 35 40 45

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Arg Leu Gln Asn Ala Ala Glu Ser Gly Leu Arg Glu Gly Glu Arg Arg
 50                      55                      60
Phe Val Asn Thr Leu Arg Pro Pro Glu Pro Gly Thr Gly Cys Thr Ala
65                      70                      75                      80
Asp Asn Val Ala Arg Pro Cys Leu Leu Asp Leu Ala Ala Leu Asn Leu
                      85                      90                      95
Lys Leu Ala Asp Thr His Gln Asn Pro Val Gly Val Leu Lys Gly Ile
                      100                      105                      110
Ala Asn Thr Trp Met Ser Tyr Arg Gly Ser Asp Ile Ser Ser Ala Thr
                      115                      120                      125
Thr Ala Gly Asn Ala Leu Gln Arg Ala Val Glu Gln Pro Ala His Ser
130                      135                      140
Leu Gly Arg Pro Gly Gln Arg Ser Gly Lys Pro Arg Ile Arg Gln Pro
145                      150                      155                      160
Asp Ala Arg His Arg His Leu Leu Leu Arg Asp Gln
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<210> 47
<211> 1161
<212> PRT
<213> Psuedomonas aeruginosa

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<400> 47
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Leu Tyr Gln Leu Ile Glu Pro Arg Met Lys Ser Val Leu His Gln Ile
                      35                      40                      45
Gly Lys Thr Ser Leu Ala Ala Ala Leu Ser Gly Ala Val Leu Leu Ser
50                      55                      60
Ala Gln Thr Thr His Ala Ala Ala Leu Ser Val Ser Gln Gln Pro Leu
65                      70                      75                      80
Met Leu Ile Gln Gly Val Ala Pro Asn Met Leu Val Thr Leu Asp Asp
                      85                      90                      95
Ser Gly Ser Met Ala Phe Ala Tyr Ala Pro Asp Ser Ile Ser Gly Tyr
                      100                      105                      110
Gly Asn Tyr Thr Phe Phe Ala Ser Asn Ser Phe Asn Pro Met Tyr Phe
115                      120                      125
Asp Pro Asn Thr Gln Tyr Lys Leu Pro Lys Lys Leu Thr Leu Val Asn
130                      135                      140
Gly Gln Val Gln Ile Gln Asp Tyr Pro Ala Pro Asn Phe Ser Ser Ala
145                      150                      155                      160
Trp Arg Asn Gly Phe Thr Arg Arg Gly Ser Ile Asn Leu Ser Asn Ser
                      165                      170                      175
Tyr Lys Val Thr Ile Glu Tyr Gly Arg Gly Tyr Asp Lys Glu Ser Thr
180                      185                      190
Ile Lys Ala Asp Ala Ala Tyr Tyr Asp Phe Thr Gly Ser Ser Ser
195                      200                      205
Trp Asn Arg Thr Asn Gln Ala Cys Tyr Thr Arg Arg Tyr Val Ser Thr
210                      215                      220
Glu Gln Arg Gln Asn Phe Ala Asn Trp Tyr Ser Phe Tyr Arg Thr Arg
225                      230                      235                      240
Ala Leu Arg Thr Gln Thr Ala Ala Asn Leu Ala Phe Phe Arg Leu Pro
245                      250                      255

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Glu Asn Ala Arg Val Ser Trp Gln Leu Leu Asn Asp Ser Asn Cys Asn
 260 265 270
 Gln Met Gly Ser Gly Ser Arg Leu Arg Gln Leu Phe Gln Gln Leu Ser
 275 280 285
 Thr Gly Leu His Arg Ser Thr Ala Gly Glu Leu Leu Gln Leu Ala Gly
 290 295 300
 Lys Thr Phe Gly Gln Trp Trp Tyr Ala Leu Arg Gln Ala Met Thr Arg
 305 310 315 320
 Glu Ala Ser Phe Ser Arg Arg Pro Ala Ser Asn Gly Pro Tyr Ala Tyr
 325 330 335
 Arg Pro Gly Thr Gln Thr Ala Pro Glu Tyr Ser Cys Arg Gly Ser Tyr
 340 345 350
 His Ile Leu Met Thr Asp Gly Leu Trp Asn Asn Asp Ser Ala Asn Val
 355 360 365
 Gly Asn Ala Asp Ser Thr Ala Arg Asn Leu Pro Asp Gly Lys Ser Tyr
 370 375 380
 Ser Ser Gln Thr Pro Tyr Arg Asp Gly Thr Phe Asp Thr Leu Ala Asp
 385 390 395 400
 Gln Ala Phe His Tyr Trp Ala Thr Asp Ala Arg Pro Asp Ile Asp Asp
 405 410 415
 Asn Ile Lys Pro Tyr Ile Pro Tyr Pro Asp Gln Asp Asn Pro Ser Gly
 420 425 430
 Glu Tyr Trp Asn Pro Arg Asn Asp Pro Ala Ile Trp Gln His Met Val
 435 440 445
 Thr Tyr Thr Leu Gly Leu Gly Leu Asn Thr Ser Leu Thr Ser Pro Arg
 450 455 460
 Trp Glu Gly Ser Thr Phe Ser Gly Gly Tyr Asn Asp Ile Val Ala Gly
 465 470 475 480
 Asn Leu Ser Trp Pro Arg Ala Ser Asn Asn Asp Ser Asn Asn Val Tyr
 485 490 495
 Asp Leu Trp His Ala Ala Val Asn Ser Arg Gly Glu Phe Phe Ser Ala
 500 505 510
 Asp Ser Pro Asp Gln Leu Val Ala Ala Phe Gln Asp Ile Leu Asn Arg
 515 520 525
 Ile Ser Gly Lys Asp Leu Pro Ala Ser Arg Pro Ala Ile Ser Ser Ser
 530 535 540
 Leu Gln Glu Asp Asp Thr Gly Asp Lys Leu Thr Arg Phe Ala Tyr Gln
 545 550 555 560
 Thr Ser Phe Ala Ser Asp Lys Asn Trp Ala Gly Asp Leu Thr Arg Tyr
 565 570 575
 Ser Leu Thr Thr Gln Asp Lys Ala Thr Val Gln Thr Asn Leu Trp Ser
 580 585 590
 Ala Gln Ser Ile Leu Asp Ala Met Pro Asn Gly Gly Ala Gly Arg Lys
 595 600 605
 Ile Met Met Ala Gly Ser Gly Thr Ser Gly Leu Lys Glu Phe Thr Trp
 610 615 620
 Gly Ser Leu Ser Ala Asp Gln Gln Arg Lys Leu Asn Arg Asp Pro Asp
 625 630 635 640
 Arg Asn Asp Val Ala Asp Thr Lys Gly Gln Asp Arg Val Ala Phe Leu
 645 650 655
 Arg Gly Asp Arg Arg Lys Glu Asn Ser Asp Asn Phe Arg Thr Arg Asn
 660 665 670
 Ser Ile Leu Gly Asp Ile Ile Asn Ser Ser Pro Ala Thr Val Gly Lys
 675 680 685
 Ala Gln Tyr Leu Thr Tyr Leu Ala Gln Pro Ile Glu Pro Ser Gly Asn

690		695		700
Tyr Ser Thr Phe Ala Glu Ala Gln Lys Thr Arg Ala Pro Arg Val Tyr				
705	710		715	720
Val Gly Ala Asn Asp Gly Met Leu His Gly Phe Asp Thr Asp Gly Asn				
	725		730	735
Glu Thr Phe Ala Phe Ile Pro Ser Ala Val Phe Glu Lys Leu His Lys				
	740		745	750
Leu Thr Ala Arg Gly Tyr Gln Gly Gly Ala His Gln Phe Tyr Val Asp				
	755		760	765
Gly Ser Pro Val Val Ala Asp Ala Phe Phe Gly Gly Ala Trp His Thr				
	770		775	780
Val Leu Ile Gly Ser Leu Arg Ala Gly Gly Lys Gly Leu Phe Ala Leu				
785	790		795	800
Asp Val Thr Asp Pro Ala Asn Ile Lys Leu Leu Trp Glu Ile Gly Val				
	805		810	815
Asp Gln Glu Pro Asp Leu Gly Tyr Ser Phe Pro Lys Pro Thr Val Ala				
	820		825	830
Arg Leu His Asn Gly Lys Trp Ala Val Val Thr Gly Asn Gly Tyr Ser				
	835		840	845
Ser Leu Asn Asp Lys Ala Ala Leu Leu Ile Ile Asp Leu Glu Thr Gly				
	850		855	860
Ala Ile Thr Arg Lys Leu Glu Val Thr Gly Arg Thr Gly Val Pro Asn				
865	870		875	880
Gly Leu Ser Ser Leu Arg Leu Ala Asp Asn Asn Ser Asp Gly Val Ala				
	885		890	895
Asp Tyr Ala Tyr Ala Gly Asp Leu Gln Gly Asn Leu Trp Arg Phe Asp				
	900		905	910
Leu Ile Ala Gly Lys Val Asn Gln Asp Asp Pro Phe Ser Arg Ala Asn				
	915		920	925
Asp Gly Pro Thr Val Ala Ser Ser Phe Arg Val Ser Phe Gly Gly Gln				
	930		935	940
Pro Leu Tyr Ser Ala Val Asp Ser Ala Gly Ala Ala Gln Ala Ile Thr				
945	950		955	960
Ala Ala Pro Ser Leu Val Arg His Pro Thr Arg Lys Gly Tyr Ile Val				
	965		970	975
Ile Phe Gly Thr Gly Lys Tyr Phe Glu Asn Ala Asp Ala Arg Ala Asp				
	980		985	990
Thr Ser Arg Ala Gln Thr Leu Tyr Gly Ile Trp Asp Gln Gln Thr Lys				
	995		1000	1005
Gly Glu Ala Ala Gly Ser Thr Pro Arg Leu Thr Arg Gly Asn Leu Gln				
	1010		1015	1020
Gln Gln Thr Leu Asp Leu Gln Ala Asp Ser Thr Phe Ala Ser Thr Ala				
1025	1030		1035	1040
Arg Thr Ile Arg Ile Gly Ser Gln Asn Pro Val Asn Trp Leu Asn Asn				
	1045		1050	1055
Asp Gly Ser Thr Lys Gln Ser Gly Trp Tyr Leu Asp Phe Met Val Asn				
	1060		1065	1070
Gly Thr Leu Lys Gly Glu Met Leu Ile Glu Asp Met Ile Ala Ile Gly				
	1075		1080	1085
Gln Val Val Leu Leu Gln Thr Ile Thr Pro Asn Asp Asp Pro Cys Ala				
	1090		1095	1100
Asp Gly Ala Ser Asn Trp Thr Tyr Gly Leu Asp Pro Tyr Thr Gly Gly				
1105	1110		1115	1120
Arg Thr Arg Phe Thr Val Phe Asp Leu Gly Arg Gln Gly Val Val Gly				
	1125		1130	1135

Leu Glu Ile Arg Leu Thr Gly Thr Thr Arg Arg Asn Val Gly Asn Pro
 1140 1145 1150
 Val Pro Ser Arg Lys Ala Trp Glu Ala
 1155 1160

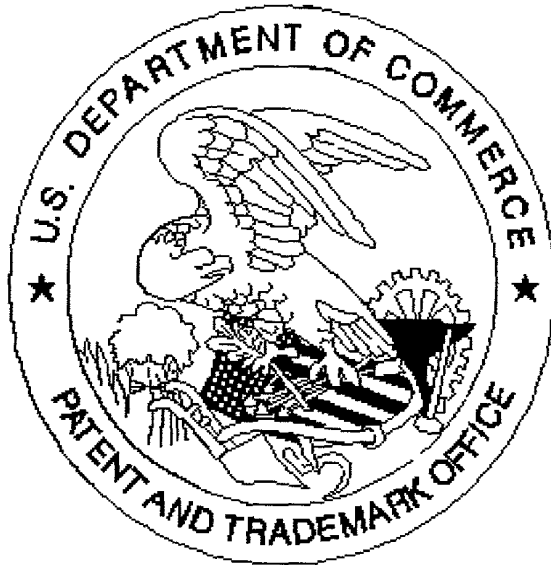
<210> 48
 <211> 115
 <212> PRT
 <213> Psuedomonas aeruginosa

<400> 48
 Met Lys Val Leu Pro Met Leu Leu Ala Leu Ala Val Pro Gly Leu Cys
 1 5 10 15
 Trp Ala Glu Asp Pro Gln Thr Phe Glu Gly Ala Gly Val Val Phe Glu
 20 25 30
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 35 40 45
 Leu Pro Asn Ser Thr Val Arg Asn Gly Met Pro Ser Leu Phe Gln Val
 50 55 60
 Lys Pro Gly Ser Val Val Ser Tyr Ser Gly Thr Val Ser Gln Pro Trp
 65 70 75 80
 Ser Thr Ile Thr Asp Ile Tyr Ile His Lys Gln Met Ser Glu Gln Glu
 85 90 95
 Leu Ala Glu Met Ile Glu Lys Glu Gln Pro Arg Gln Asp Gly Glu Glu
 100 105 110
 Gln Pro Arg
 115

<210> 49
 <211> 141
 <212> PRT
 <213> Psuedomonas aeruginosa

<400> 49
 Met Arg Thr Arg Gln Lys Gly Phe Thr Leu Leu Glu Met Val Val Val
 1 5 10 15
 Val Ala Val Ile Gly Ile Leu Leu Gly Ile Ala Ile Pro Ser Tyr Gln
 20 25 30
 Asn Tyr Val Ile Arg Ser Asn Arg Thr Glu Gly Gln Ala Leu Leu Ser
 35 40 45
 Asp Ala Ala Ala Arg Gln Glu Arg Tyr Tyr Ser Gln Asn Pro Gly Val
 50 55 60
 Gly Tyr Thr Lys Asp Val Ala Lys Leu Gly Met Ser Ser Ala Asn Ser
 65 70 75 80
 Pro Asn Asn Leu Tyr Asn Leu Thr Ile Ala Thr Pro Thr Ser Thr Thr
 85 90 95
 Tyr Thr Leu Thr Ala Thr Pro Ile Asn Ser Gln Thr Arg Asp Lys Thr
 100 105 110
 Cys Gly Lys Leu Thr Leu Asn Gln Leu Gly Glu Arg Gly Ala Ala Gly
 115 120 125
 Lys Thr Gly Asn Asn Ser Thr Val Asn Asp Cys Trp Arg
 130 135 140

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